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Result
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Perfect score:
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      seq length: 0 seq length: 2000000000
      Match
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                                             2156
2303
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425
427
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1100
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US-08-347-594A-1
US-08-463-682-2
US-08-841-349-1
US-08-26-426B-248
US-08-25-426B-248
US-08-25-426B-7
US-08-461-136C-25
US-08-461-136C-25
US-08-478-507-12
US-08-478-507-12
US-08-478-507-1
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US-08-478-507-1
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US-09-128-275A-1
US-09-128-275A-1
US-09-128-275A-1
US-09-331-924-1
US-08-102-863-10

PCT-US92-10885-10

US-09-311-924-3

US-08-959-011-2

US-08-480-229C-9

US-08-480-229C-28

US-08-480-229C-28
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Sequence 25, Appl
Sequence 12, Appl
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CURRENT APPLICATION NUMBER: US/09/437,457
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8

LENGTH: 230
TYPE: DNA
ORGANISM: Homo sapiens

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ALIGNMENTS	PCT-US95-06420-1 US-07-745-206A-14 US-08-311-363-14 US-09-173-914-35 US-08-981-729-9 US-08-981-4468-2 US-08-981-4468-2 US-08-981-4468-2 US-08-981-468-1 US-08-986-485-1 US-08-986-485-1 US-08-311-363-12 US-08-311-363-12 US-08-456-2008-11 US-08-665-259-19 US-08-456-543A-8 US-08-455-543A-8 US-08-453-078B-8	US-08-247-946A-1
	Sequence 1, Appli Sequence 14, Appl Sequence 35, Appl Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli	Sequence 1, Appli

RESULT 1 US-09-437-457-8

GENERAL INFORMATION:

APPLICANT: Giordano, Anthony
APPLICANT: Xavier, Ashish
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
TITLE OF INVENTION: INVERACTIONS AND MRNA FUNCTIONALITY
FILE REFERENCE: 50093/014001

Sequence 8, Application US/09437457 Patent No. 6273893

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US-08-347-594A-1/c
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; Patent No. 5849536
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Best Local 9
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APPLICANT: Garfinkel, Leonard
APPLICANT: Richter, Tamar
                                                                                                                                                 APPLICANT: Righter, Tamar TITLE OF INVENTION: CLONIN TITLE OF INVENTION: WILLER TITLE OF INVENTION: METHOL
                 COMPUTER READABLE FORM:
                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  166 GTCCGCCCGCTGAGG 180
                                 COUNTRY:
                                                                        CITY:
MEDIUM TYPE: Floppy disk
                                                            STATE:
                                                                                          STREET:
                                                                                                      ADDRESSEE:
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                                                          New York
: New York
                                  10036
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                                                                                        E: John P. White
1185 Avenue of the Americas
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                                            USA
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Pred. No. 19;
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US-08-463-682-2/c
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              INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 6153 base pairs
TYPE: nucleic acid
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                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                     REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
STRANDEDNESS: single
                                                                          TELEFAX:
                                                                                                                                                                                           FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                        TELEPHONE:
                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                          APPLICATION NUMBER:
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STRANDEDNESS: single
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Y: U.S.A.
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                                                                       : (212) 278-0400
(212) 391-0525
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; LOCATION: (1674)..(2069)
US-08-841-349-1
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                                                                                                                                                                                                                                                                                                     Patent No. 5558988
GENERAL INFORMATION:
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LENGTH: 5434
                                                                                                                                                                                                                                                                                                                                       Sequence 248, Application US/07977284A
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Best Local (
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CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: For all n's in this sequence, n=(a or g or c or t)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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COMPUTER READABLE FORM:
                                                                                                                              APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRIT
NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                                                                                                                                                                                                                          1421 GTCCGCCCGCTGCGG 1435
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ANTI-SENSE: N
FEATURE:
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                  ZIP:
                              COUNTRY:
                                                  STATE:
                                                           STREET: One Liberty Place, 46th floor CITY: Philadelphia
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LOCATION:
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Williams, Charlene J.
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93.3%;
                                                                                                                                                PREDISPOSITION FOR OSTEOARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.4; DB 2;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5948611 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 248,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 248
PRIOK AFFILIATION NUMBER: PCT/US93/1000
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,284
                                                              CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: PCT/US93/10964
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Prockop, Darwin J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                     APPLICATION NUMBER: US/08/256,426B FILING DATE: 03-FEB-1995
                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: WORDPER
                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                CITY: Philadelphia
                                                                                                                                                                                                                                                      ZIP: 19103
                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 CCGCCCGCTGAGG 45
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                      Hopkinson, Ian
Ahmad, Nilofer Nina
VENTION: Methods of Detecting A Genetic
                                                                                                                                                                     SYSTEM: Windows 3.1
WORDPERFECT 6.1
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Williams, Charlene J.
                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                     IBM Compatible
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100.0%; Pred. No.
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; Patent No. 5891695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                         TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/FR 93/00923 FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA: POLICATION DATA: POLICATION DATA: POLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         SEQUENCE CHARACTERISTICS:
                                                                                               REFERENCE/DOCKET NUMBER: 03806.0054-00000 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: De Crecy-Lagard, Valerie TITLE OF INVENTION: Polypeptides InvITLE OF INVENTION: Biosynthesis of TITLE OF INVENTION: Coding For These
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                                                                                                                             REGISTRATION NUMBER: 25,146
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                                                                                                                                                          NAME:
                                                                                                                                                                                                           APPLICATION NUMBER: FR 92/11441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                      Meyers, Kenneth
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695 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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b. 2.1e+02;
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US-08-510-646B-7
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                                                                                                                                 FILING DATE: 10-MAY-1995
PRIOR APPLICATION NOMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
             REFERENCE/DOCKET NUMBER: 03806.0054-01000 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
                                                                                         APPLICATION NUMBER: FR 9:
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides and Their Use
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
TELEFAX: (202) 408-4400
                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                           COMPUTE ?:
                                                                           NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /product= "Gene Snac"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: S.pristinaespiralis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crouzet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blanche, Francis
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212..695
                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zagorec, Monique
Debussche, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lacroix, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacques, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blanc, Veronique
                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        FR 92/11441
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                                                         25,146
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Pred. No.
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                                                                                                                 FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                     FILING DATE: 25-SEP-PRIOR APPLICATION DATA:
                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cD
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LENGTH: 695 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                          REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/OR APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1300 1 CITY: Washington
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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OTHER INFORMATION:
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1300 I Street, N.W., Suite 700
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Zagorec, Monique
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(202) 408-4000
                                                                                                                                                                                   UMBER: FR 92/11441
25-SEP-1992
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100.0%; Pred. No. 1.9e+02;
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                                                                                           TELEPHONE: 212-867-01:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
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            MOLECULE TYPE:
                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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FEATURE:
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                           TOPOLOGY:
                                       STRANDEDNESS:
                                                      TYPE:
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 43
                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                  LENGTH:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                 10174-640
                                             : 425 base pairs nucleic acid
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INVENTION: No. 600
                                                                                                                                                                                                                                                                                                                                                                         New York
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                                                                                                                                                                                                                                                                                                                                                                                                  405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     695 base pairs
                                                                                                                                                                                                                                                                                                                                                            United States of America
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Ihara, Michiko
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Lassen, Soren F
                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schulein, Martin
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                                   TELEFAX: (650) 324-09
INFORMATION FOR SEQ ID NO:
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                      SEQUENCE CHARACTERISTICS:
                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                            FILING DATE: 17-JUN-1988 ATTORNEY/AGENT INFORMATION:
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MEDIUL HYPE: Floppy
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APPLICATION NUMBER: 1
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA Sequences of Enterically Transmitted TITLE OF INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
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      LENGTH:
                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                    NAME: Sholtz, Charles REGISTRATION NUMBER: 3
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                                                                  TELEPHONE:
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874 base pairs
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Yarbough, Patrice O
Bradley, Daniel W
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                                                                  (650) 324-0880
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92.9%;
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                                                                                                                                                                                 US 07/208,997
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                                                                                                                  38,615
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Pred. No. 3.9e+02;
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US-09-128-275A-12/c

: Sequence 12, Application US/09128275A

: Patent No. 6229005
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                                                   ATTORNEY/AGENT INFORMATION:
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
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APPLICANT:
                                                                                                                                            FILING DATE: 16-JUN-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICANT:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                   NAME: Petithory, Joanne R. REGISTRATION NUMBER: 42,99
REFERENCE/DOCKET NUMBER: 46
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 03-AUG
                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                             APPLICATION NUMBER:
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EDNESS: double
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Yarbough, Patrice O
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Fry, Kirk E
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Bradley, Daniel W
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92.9%;
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Best Local Similarity 92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 324-0960 INFORMATION FOR SEQ ID NO: 12:
            REFERENCE/DOCKET NUMBER: Bayer 8398.3-KGB TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
                                                                                                                                            APPLICATION NUMBER: 08/0 FILING DATE: 19-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Franz, Jurgen; Weingartner, Bernhard;
APPLICANT: Unterbeck, Axel; Rae, Peter
TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
TITLE OF INVENTION: THEIR USE
                                                                                                APPLICATION NUMBER: DE 4
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              SUFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 874 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 TCCGCCCGCTCAGG 840
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/09
FTI.ING DATE: 19-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
STATE:
TELEFAX:
                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 10591-5144
                                                                                    NAME:
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB MEDIUM TYPE: storage
                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                    Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08456200B
(914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      NEC Powermate SX/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPRUNG HORN KRAMER & WOODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO
                                                                                                                                                                                                                   26-MAR-1992
                                                                                                                                                                                                                                                                                                                                     31-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                      DOS
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                                                                                                                                                                                08/064,778
                                                                                                                                                                                                                                                                                    08/094,712
                                                                                                                                  DE 41 10 785
                                                                                                                                                                                                                                    07/858,278
                                                                                                                                                                                                                                                                                                                                                   US/08/456,200B
                                                               33,141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 4; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 874;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-456-200B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08478507; Patent No. 6120988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 1100 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
TELECOMMUNICATION INFORMATION:
                                                            FILING DATE: 17-JUN-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                           FILING DATE: 11-APR-:
PRIOR APPLICATION DATA:
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-JUL-PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DNA Sequences of Enterically Transmitted TITLE OF INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
            NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                              APPLICATION NUMBER: US 07 FILING DATE: 13-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 906 TCCGCCTGCTGAGG 919
                                                                                             APPLICATION NUMBER:
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krawczynski, Krzysztof z
Tam, Albert
Fry, Kirk E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yarbough, Patrice
Bradley, Daniel W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reyes, Gregory R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dehlinger & Associates
                                                                                                                              11-APR-1989
                                                                                                                                                                                                                                                                                                                                 05-APR-1991
                                                                                                                                                                                                                                                                                                                                                                               25-JUL-1994
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92.9%;
                                                                                                                                              US 07/336,672
                                                                                                                                                                                                                                                                                                                                                                                            US 08/279,823
                                                                                             US 07/208,997
                                                                                                                                                                                                                                             US 07/420,921
                                                                                                                                                                                                                                                                                                                                           US 07/681,078
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                             38,615
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             4600-0183.22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.4; DB 4;
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1100;
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US-08-478-507-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                     APPLICATION NUMBER: FILING DATE: 05-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                               FILING DATE: 25-JUL-1994 PRIOR APPLICATION DATA:
FILING DATE: 05-APR-
PRIOR APPLICATION DATA
                                                                                                                          FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1112 TCCGCCCGCTCAGG 1099
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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NAME/KEY:
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INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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                                                                                                                                                                                                                                                          ZIP:
                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            APPLICATION NUMBER:
                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                  STREET:
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LOCATION:
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TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                            94306
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                                                                                                                                                                                                                                                                                                             350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1295 base pairs
                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                   Tam, Albert
Fry, Kirk E
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradley, Daniel W
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reyes, Gregory R
Yarbough, Patrice O
                                                                                                                                                                                                                                                                                                                                                                                                                             Krawczynski, Krzysztof Z
                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO
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3..1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2..1294
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            05-APR-1990
                                                      05-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                                                         DNA Sequences of Enterically Transmitted No. 6120988-A/No. 6120988-B Hepatitis Viral Agent; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%;
                                                                   us 07/681,078
                                                                                                            US 08/279,823
                                                                                                                                                        US/08/478,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.33 kb EcoRI insert of ET1.1, forward sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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APPLICATION NUMBER: US 07/420,921

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/357,486

FILING DATE: 16 -JUN-1989

PRIOR APPLICATION NUMBER: US 07/336,672

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997

TELEPOWER/ACT ON NUMBER: US 07/208,997

TELEPOWER/ACT
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Result
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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Copyright (c) 1993 - 2002 Compugen Ltd.
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gb_est2:*
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BF709326
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BI404045
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                        BE245562
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          BF709326 MI-P-AY0-
BG733337 347192 MA
BE245562 TCBAP1E21
BF708610 MI-P-AY0-
                                                                                               BI402471 MI-P-CP0-
BG733338 347193 MA
BE235921 143549 MA
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                                                              BI401388 MI-P-CP0-
BG610493 326435 MA
BF708610 MI-P-AY0-
BI401812 MI-P-CP0-
                                                       BI399086 MI-P-AY1-
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## ALIGNMENTS

KEYWORDS SOURCE RESULT 1 BI401298 COMMENT REFERENCE ACCESSION LOCUS VERSION DEFINITION JOURNAL TITLE ORGANISM AUTHORS Email: ckluggle@lastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized uterus library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com) BI401298 287 bp mRNA linear EST MI-P-CPO-nvm-d-02-0-UI.sl MI-P-CPO Sus scrofa cDNA clone MI-P-CPO-nvm-d-02-0-UI 3', mRNA sequence. POLYA=Yes. Contact: Tuggle CK Molecular Genetics Laboratory, Department of Animal Science Iowa State University 201 Kildee Hall, Ames, IA 50011-3150, USA 97044477 Genome Res. 6 (9), 791-806 (1996) Bonaldo, M.F., Lennon, G. and Soares, M.B. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 287) BI401298 Normalization and subtraction: two approaches to facilitate gene Sus scrofa BI401298.1 GI:15180359 BI401298 5152942401 EST 14-AUG-2001

FEATURES

source

Location/Qualifiers
1. .287
/organism="Sus scrofa"
/db\_xref="taxon:9823"

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 bp mRNA linear EST. MI-P-AX1-nrp-g-06-0-UI.sl MI-P-AX1 Sus scrofa cDNA clone MI-P-AX1-nrp-g-06-0-UI 3', mRNA sequence.
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201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tuggle CK
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY1 polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AY1 polylinker; Site_1: Not I; Site_3: EcoRI; The MI-P-AY1 polylinker; Site_1: Not I; Site_3: EcoRI; The MI-P-AY1 polylinker; EcoRI; The MI-P-AY1 polylinker; EcoRI; EcoRI; The MI-P-AY1 polylinker; EcoRI; 
                                                                                                                                                                                                                                                                                                                  /strain="crossbreed"
                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
library is normalized library derived from the MI-p-AYO
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site at http://pigest.genome.iastate.edu/.The procedure used to create this library has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH108 (Life Technologies)"
/lab_host="DH108 (Life Technologies)"
/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0
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/clone_lib="MI-P-CPO"
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291 bp mRNA linear EST MI-P-CP1-nwv-f-11-0-UI.S1 MI-P-CP1 Sus scrofa cDNA clone MI-P-CP1-nwv-f-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cktuggle@iastate.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 Kildee Hall, Ames, IA 50011-3150, USA
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library is normalized library derived from the MI-P-CPO library, ultimately derived from uterus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at http://piqest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996) TAG_SEQ=None found*
                                                                                                                                                                                                 /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP1
                                                                                                                                                                                                                                                                      /db_xref="taxon:9823"
/clone="MI-p-CP1-nwv-f-11-0-UI"
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                                                                                                                                                                                                                                                                                                                                                          /strain="crossbreed"
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Pred. No. 1.6e+03;
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Best Local Similarity Matches 15; Conserv
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1 (bases 1 to 295)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cktuggle@iastate.edu

Email: cktuggle@iastate.edu

The sequence contained an oligo-dm track that was present in the

Sequence contained an oligo-dm track the synthesis of first

The sequence contained and used to prime the synthesis of poly A

oligonucleotide that was used to prime the synthesis of poly A

oligonucleotide that was used to prime the synthesis the Noti site

strand cDNA and therefore this may represent a bonafide poly A

tall The sequence tag present in the cDNA between the Noti site

and the oligo-dm track served to verify it as a clone from the

non-normalized uterus library cDNA Library preparation: M.B. Soares

and the oligo-dm track served to verify it as a clone from the

non-normalized uterus library cDNA Library preparation: M.B. Soares

non-normalized uterus library contains M.B. Soares Lab, University

of lowa Clone distribution: clones will be available through

of lowa Clone distribution:
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201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
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/db_xref="taxon:9823"
/clone="MI-P-CPO-nv1-c-03-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                     visit our web site at http://pigest.genome.iastate.edu/.
The procedure used to create this library has been
previously described (Bonaldo, Lennon and Soares, Genome
previously described (Bonaldo, Lennon and Soares)
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71 c 89 g
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                                                      100.0%; score 15; DB 10;
100.0%; pred. No. 1.6e+03;
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236 GTCCGCCGCTGAGG 250
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201 Kildee Hall, Ames, IA 50011-3150, USA
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The procedure used to create this library has been
The procedure used to create this library has been
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previously described (Bonaldo, Lennon and Soares, Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CPO library is derived from uterus. For a detailed description of the library from which this clone was derived, please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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The procedure used to create this library has been
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                                                                                            Tel: 402 762 4366
Fax: 402 762 4390
PCR PRimers
                                                                                                                                     PO Box 166,
                                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                        and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                             EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                 BE235921.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE235921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 109 row: 0 column: 24
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:9020639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 328)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE235921 328 bp mRNA linear 143549 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 310)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
100 c 85 g 73 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                      Clay Center, NE 68933-0166, USA
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Pred. No. 1.6e+03;
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ORIGIN
                                                                                  BASE COUNT
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BG895911/c
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Best Local Similarity
                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 356)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett C.*
                                                                                                                                                                                                                                                                                          Plate: 124 row: H column: 11 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred w0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                             and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Keele, J.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG895911.1 GI:14306152
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                                                                   /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

69 c 66 g 64 t
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3 100 c 83 g 73 t
                                                                                                                                                                        /tissue_type="pooled"
                                                                                                                                                                                                                                 /organism="Sus scrofa"
                                                                                                                                                                                              /clone_lib="MARC 1PIG"
                                                                                                                                                                                                                 /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                         /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 15; DB 9; 100.0%; Pred. No. 1.6e+03;
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  Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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              Length 336;
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ORIGIN
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AUTHORS
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                                              Matches
                                                                      Best
                                                                                        Query Match
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                                                                   Local
1 GTCCGCCCGCTGAGG 15
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                                            l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oli onucle tide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized uterus library cDNA Library Preparation: M.B. Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 5152944252
Fax: 5152942401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cktuggle@iastate.edu
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Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                            Conservative
                                                                                                                                                     TAG_TISSUE=uterus
TAG_SEQ=AGTCCAATCG"
98 c 103 q
                                                                                                                                                                                                                                                                                 visit our web site at http://pigest.genome.iastate.edu/. The procedure used to create this library has been
                                                                                                                                                                                                                                                                                                                           /lab_host="DH108 (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-CP0 library is derived from uterus. For a detailed description of the library from which this clone was derived, please
                                                                                                                                                                                                                    TAG_LIB=MI-P-CPO
                                                                                                                                                                                                                                       previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="MI-P-CP0-nvk-f-07-0-UI"
/clone_lib="MI-P-CP0"
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                                                          Score 15; DB 10;
Pred. No. 1.6e+03;
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241 GTCCGCCCGCTGAGG 255

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LOCUS
DEFINITION
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BG610493/c
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TITLE
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                                                                                                                                                                                                                                                    MI-P-AY1-nrk-b-07-0-UI.sl MI-P-AY1 Sus scrofa cDNA clone MI-P-AY1-nrk-b-07-0-UI 3', mRNA sequence.
Contact: Tuggle CK
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                               Genome Res. 6 (9), 791-806 (1996)
                                                           Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                BI399086
                                                     discovery
                                                                                         Bonaldo, M.F.,
                                                                                                                                 Mammalia;
                                                                                                                                                   Eukaryota;
                                                                                                                                                                   Sus scrofa
                                                                                                                                                                                                                        BI399086.1 GI:15178147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACKWARD: GTTTTCCCAGTCACGACG
Plate: 101 row: D column: 20
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and _minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
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BG610493.1 GI:13660472
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                                                                                                                       Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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/clone_lib="MARC 1PIG"
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/lab_host="DH10B"
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                                                                                                                                       Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                       Lennon, G. and Soares, M.B.
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Local Similarity 100.0%; Pred. No. 1
                Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5153944252
                                                                                    Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                     Contact: Tuggle CK
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                                                                                                                                                      97044477
                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 393)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
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                                                                                                                                                                                                          discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                          BF709326.1 GI:12008803
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201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 5152942401
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112 c 10
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TAG_LIB=MI-P-AY1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DHIOB (Life Technologies)"
/note="Vector: pTT73D-Pac (Pharmacia) with a modified
/note="Vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Econ; The MI-P-AY0
library is normalized library derived from the MI-P-AY0
library, ultimately derived from placenta tissue. For a
detailed description of the library from which this clone
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/db_xref="taxon:9823"
/clone="MI-P-AYI-nrk-b-07-0-UI"
/clone_lib="MI-P-AYI"
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                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                               Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG733337 406 bp mRNA linear 347192 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
  Plate: 109
                       BACKWARD: GTTTTCCCAGTCACGACG
                                                                       PCR PRimers
                                                                                                                                                                   Email: smith@email.marc.usda.gov
                                                                                                                                                                                               Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                       and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG733337.1 GI:14019621
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                                                 FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                              EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYA=Yes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived, please visit our web site at http://piest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-AYO library is derived from placenta. For a detailed description of the library from which this clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE~placenta
TAG_SEQ~ATTGG"
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/db_xref="taxon:9823"
/clone="MI-P-AYO-nah-c-09-0-UI"
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column: 23
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Pred. No. 1.7e+03;
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BE245562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GTCCGCCCGCTGAGG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Citation: Carninci, P. and Hayashizaki, Y. High efficiency full length cDNA cloning. Methods Enzymol. 303, 19-44 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE245562 406 bp mRNA linear EST 03-OC: TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: clones@txccc.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pediatric Leukemia cDNA Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE245562.1 GI:9097308
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inote="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GAAGGACTGAACGGCGCAAGGAGGT)YN 3'; V=A,C,G; N-A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AAGAGACTGCGGATCAGATAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SaII sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN
                                                                                                                                                                                                                                        /cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

a 116 c 108 g 93 t
                                                                                                                                                                                                                                                                                                                                                               leukemia Baylor-HGSC project=TCBA"
                                                                                                                                                                                                                                                                                                                  /tissue_type="leukopheresis"
                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Pediatric pre-B cell acute lymphoblastic
                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="TCBAP2132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/lab_host="DH10B"
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/clone_lib="MARC 1PIG"
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    Mismatches

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Pred. No.
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                                                                                                                                                  CCCCGCCGTGGGTCCGCCTG 176
Human gene for beta-adrenergic receptor (beta-2 subtype)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 178203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., García,
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., García,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                            HSBAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 2063)
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SGLTSELPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSEYVPLVINVFV
                                                                                                                                                                                                                                                                                                                                                                                                 TVPSDNIDSPGRNCSTNDSLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mgQpgngsafllapngshapdhDvTQQRDEVWVVGMGIVMSLIV
LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMVTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="MGC:21367 IMAGE:4538187"
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                                                                                                                                                                                                                                                                                                                                                                                                                           AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAH12481.1"
/db_xref="GI:15214694"
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                                                                                                                                                                                                                                                                         92.0%;
95.0%;
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           Sequence 1 from Patent W09937761
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEYYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFYGHQG
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                                                                                                                                                                                                                                                                                                                                              /note="
1712. .
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896. .967
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NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                                                                                                                                                                                                                                                                                                           /note="membrane spanning domain VII"
616 c 649 g 545 t
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="membrane spanning domain IV" 1385, .1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="membrane spanning domain III"
1247. .1315
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                                                                                                                                                                                                                                                                                                                                                                                              'note="membrane spanning domain V"
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95.0%;
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Pred. No. 5.8e+02;
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Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

    nucleic search, using sw model

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Copyright (c) 1993 - 2002 Compugen Ltd
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AAK00425 AAK25868 AAI10498 AAI31752	0 4 FD (	AAC25379 AAAS1079 AAH27139	AAT55178 AAA95743 AAL31694 AAH79739	AAT55545 AAT55356 AAT53180 AAT53133	AAF54045 ABL18856 AAA38786 AAV30491	781 465 268 170	AAS42187 AAK69784 AAQ29269 AAQ37818 AAQ84658 AAV42686 AAA71704 AAV29059
Human brain expres Human bone marrow Probe #431 for gen Probe #438 used to	cDNA 3 foetal #419 f	FLINT PCR prd primer fo	relA pha pr SNP o	Human relA hammerh Human relA hammerh Mouse ICAM hammerh Mouse ICAM hammerh		nce encod neuronal ncoding h calcium e calcium	Genomic sequence # Human immune/haema Human calcium chan Sequence encoding Human neuronal cal DNA encoding human Human calcium chan

## ALIGNMENTS

Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; Liggett SB: (UYCI-) UNIV CINCINNATI. 25-NOV-1998; 24-NOV-1999; 02-JUN-2000 WO200031307-A1 Homo sapiens allele-specific oligonucleotide probe; ss. Human beta2 adrenergic receptor beta2AR T allele-specific probe 05-OCT-2000 AAA38787 standard; DNA; 15 BP. (first entry) 98US-0109886. 99WO-US27963.

WPI; 2000-400107/34.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlphalB-adrenergic receptor; human; cardiovascular disease; beta2 adrenergic receptor; genetic variation identification; hypertrophy; disease diagnosis; hypertension; prostatic disease; pulmonary disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and determine the best treatment.
This sequence represents the human beta2-adrenergic receptor gene, and is amplified by the primers of the invention. The primers are non-self hybridising; contain at least 15 nucleotides (nt) and has a melting
                                                                          Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                         Buescher R,
                                                                                                                                                                                                                                                                                                                                                                                                                                              endocrine-metabolic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta2-adrenergic receptor gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 1 A; 5 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 asthma, hypertension, congestive heart failure, i arrhythmia, obesity, diabetes, vascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is an allele-specific oligonucleotide probe for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                           Pairs of oligonucleotides for amplifying adrenergic receptor genes
                                                                                                                                                                                                                                                                10-NOV-1997;
                                                                                                                                                                                                                                                                                                   04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                       20-MAY-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX61116 standard; DNA; 2300 BP
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                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral vascular disorder; neuropsychic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                              97US-0086232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  congestive heart failure, ischemic heart disease,
                                                                                                                                                                                         Insel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 21;
Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disease, hypertension and asthma, but variations may also be associated with peripheral vascular, pulmonary, neuropsychic and endocrine-metabolic disorders. These primers allow rapid and specific amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous gene segments of the alphalB and amplification of large and homogeneous generation of large 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta2 genes from a complex mixture of DNAs. This makes possible detection of genetic alterations not previously amenable to routine, automated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alphalB gene are associated with cardiovascular disease, hypertension and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-adrenergic receptor-2 gene; coding region; polymorphism; polymorphic marker; cardiovascular disease; myccardial infarction; unstable angina; hypertension; atheros stroke; prognosis; drug screening; treatment outcome; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA38340 standard; DNA; 2305 BP
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                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-318010/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EURO-) EURONA MEDICAL AB
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14-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta-adrenergic receptor-2 coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0104302.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindstrom PHR,
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Pred. No. 1.9e+0?
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status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (ATI) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one

The invention relates to a novel method of assessing the cardiovascular

Disclosure; Page 124-125; 126pp; English. encoding specific proteins, with reference

Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes

polymorphic pattern

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. The present sequence represents the human beta-ademergic receptor 2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results an early trial can be evaluated tidentify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or elaminates trial and error in selecting a treatment for a particular individual cardiovascular patient. It also provides the ability to
                         mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding region (GenBank Y00106/g293708). The polymorphic sites identified are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
                                                                                                                                                                                                                                                                                                                                   neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                                                                                                                                                                                                                                                                                                                                                       neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta 2-adrenergic receptor DNA variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ00774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ00774 standard; DNA; 3451 BP
                                                                                                                       mutation
                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                       metabolic illness; gene therapy; pharmaceutical intervention therapy
                                                                                                                                                                                                                                                                                                                 post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740 GICCGCCTGCTGAGG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTCCGCCTGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no insert/G/C and 2070 no insert/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                       replace(245,a)
                                    /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
                                                                                                                    replace(159,t)
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 15; DB 21; Length 2305; 100.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation
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                    30-DEC-195c;
                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                      mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation
                                                                   29-JUL-199"
                    98WO-DE03818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AA200773 and results in a change in the corresponding wild type amino acid sequence from an Glu residue to Gln residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(1633,a)
/*tag= i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(934,g)
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AA200773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(2078,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(1839,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(1221,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(1120,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(565,g)
                                                                                                                                                                                          /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                      replace(2826,g)
                                                                                                                                                                                                                                                                                       /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                        replace(2640,g)
                                                                                                                                                                                                                                                                                                                                                                                         /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(2110,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(1666,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1568,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence represented in AA200773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence represented in AAZ00773*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AA200773 and results in a change in the corresponding wild type amino acid sequence from an Ile residue to Thr residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wild type amino acid sequence from an Cys
residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence represented in AAZ00773'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and results in a change in the corresponding wild type amino acid sequence from an Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequence represented in AAZ00773
                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AAZ00773*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid sequence represented in AA200773'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AA200773*
                                                                                                                                                             sequence represented in AAZ00773'
                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                represented
                                                                                                                                                                                                                                                                in AAZ00773"
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g 99

97DE-1058401

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RESULT 5
AAZO0775
ID AAZO
XX AAZO
AC AAZC
XX AAZO
DT 07-(
XX Bet
KW Bet
KW Ca;
KW Ca;
KW Ca;
KW Po
KW Po
KW Po
KW Po
KW Po
KW Be
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FT FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including mycoardial infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be
                                                                                                                                                                                                                                                            neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                           neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depress)on;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA200775 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1534 GTCCGCCTGCTGAGG 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 2a; 27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                         Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                        mutation
                                                                                                                                                     Synthetic.
                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                            metabolic illness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GTCCGCCTGCTGAGG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                  2-adrenergic receptor DNA variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes novel variant human beta 2-adrenergic receptor
                                                                                      replace(1541,c)
                                                                                                             Location/Qualifiers
                                                                 /*tag=
                                                                                                                                                                                                                                       gene therapy; pharmaceutical intervention therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Timmermann B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
"This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773
and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 20;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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and Riley- y syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                  predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                          anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the auto comous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                                                                                                                                                                                                                                                                                                                                                                                          gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 2a; 27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09937761-A1
                                                                                                                                                                                                                                                                                                        determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                         2-adrenergic receptor gene which is represented in AAZ00773.
                                                           individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta
                                                                                                                                                                                                                                                                                                                                                                          for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-479048/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koepke K, Timmermann B;
                                                                                                                                                                                                                                                                                                                                                 infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97DE-1058401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wild type amino acid sequence from an residue to Arg residue"
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Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

Matches Local <u>ب</u> 5: Similarity Conservative 100.0%; Score 15; DB 20; 100.0%; Pred. No. 1.9e+02; 0; Mismatches 0; Length 3451; Indels 0, Gaps 0;

Qy 밁 1534 GTCCGCCTGCTGAGG 1548 1 GTCCGCCTGCTGAGG 15

AAZOO777 Human beta 2-adrenergic receptor DNA variant 4. 07-OCT-1999 AAZ00777; AAZ00777 standard; DNA; 3451 (first entry)

neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; metabolic illness; gene therapy; pharmaceutical intervention Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;

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ğ
                                                                                                                                                       Matches
  1534 GTCCGCCTGCTGAGG 1548
                                                                                                                                                                                                                                                                                                       anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having sective nordernergic-reeptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be
                                                                                                                                                                                                                                                                                                                                                                                                                        myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxioattention deficit disorder with hyperactivity, eating disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                     determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                       Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 2a; 27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human beta2-adrenergic receptor gene variants, useful for determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-479048/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoehe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998;
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                                                                                               POCGI
                                    1 GTCCGCCTGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention describes novel variant human beta 2-adrenergic receptor
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koepke K,
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DE-1058401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-DE03818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773
and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1541,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This nucleotide differs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Timmermann B;
                                                                                             100.0%; Score 15; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wild type amino acid sequence from an Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue to Arg residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wild type amino acid sequence from an Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residue to Arg residue"
                                                                           0; Mismatches
                                                                                             1.9e+02;
                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from the wild
                                                                                                              Length 3451;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases, including
                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                anxiety,
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AAZ00778

AAZ00778 standard; DNA; 3451 BP

Query Match Matches

Local Similarity

100.0%; Score 15; 1 100.0%; Pred. No. 1

DB 20; .9e+02;

Length 3451;

0; Gaps

0;

Conservative

0

Mismatches

Sequence 3451 BP;

790 A; 872 C; 895 G; 894 T; 0 other;

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gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular disease, including myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulinia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and kiley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traum tic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                  individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                             predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                     disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoehe M, Koepke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolic illness; gene therapy; pharmaceutical intervention therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human beta 2-adrenergic receptor DNA variant 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-OCT-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel variant human beta 2-adrenergic receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wild type amino acid sequence from an Cys
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of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
                                                                                                This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as
                                                                                                                                                                                             Claim 8; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity;
                                                                                                                                                                                                                                                                                     WPI; 1999-479048/40
                                                                                                                                                                                                                                                                                                                       Hoehe M,
                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation
                                                                                                                                                                                                                                                                                                                                                      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
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                                                                                                                                                                                                                                              beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                                                                                                                                                                                                                                                                                     Koepke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         97DE-1058401
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                                                                                                                                                                                                                                                                                                                    Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence represented in \mathtt{AAZ00773} and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wild type amino acid sequence from an Gly residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wild type amino acid sequence from an Cys residue to Arg residue"
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                          calcium flux assays to screen for neurone-specific calcium channel ligands
                                                    Cloned human neuronal calcium channel sub-types - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used
                                                                                                                        Franz J,
                                                                                                                                                    (FARB ) BAYER AG
                                                                                                                                                                              04-APR-1991;
                                                                                                                                                                                                          23-MAR-1992;
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                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                           misc_difference 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human calcium channel 27980/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ29275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ29275 standard; DNA; 1100 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                 P-PSDB; AAR27655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                             1992-333446/41.
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                                                                                                                       Rae P,
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1037..1
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                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "undefined"
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                                                                                                                       Unterbeck A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred. No. 1.9e+02;
                                                                                                                     Weingaertner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3451;
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Claim 2; Page 96-98; 101pp; German

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RESULT 10

AAS42187

ID AAS422

XX AAS42

AC AAS42

XX 1190

AC Genom

XX Human

KW Ligas

KW Ligas

KW Ligas

KW AD100

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KW AD100

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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                            18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neuroblastoma cell line, hippocampus, frontal and temporal cortex and visual cortex cDNA banks were screened with a probe containing carp skeletal muscle Ca-channel cDNA. The cDNA c/one pRR14-35 is 3400bp long; the 5′1100bp were seguenced and found to overlap the clone pR14-5.3.3.1 (see AAQ29269). The sequence can be inserted into a eukaryotic expression vector for use in transforming suitable host cells. Cell lines producing human neuronal calcium channel proteins can be used for screening for Ca channel ligands (agonists or antagonists). See also AAQ29259-Q29274.
                                                                                                                                                                                                                            07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      blood-related disorder; infectious disorder; gene therapy; cytostatic;
anti arthritic; nephrotropic; anticoagulant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; autoimmune disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence #503 encoding novel human enzyme polypeptide.
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ilarity 100.0%;
Conservative (
       2000US-0225214.
2000US-0225266.
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Pred. No.
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26-SEP-
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2000US-0239937.
2000US-0240960.
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17-NOV-2000;
                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                        (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polypucieotides of the invention can also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention.
                                                                                                                                                                                                                                  disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human enzyme polypeptides (AAUZ2915-AAUZ3814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                            diagnosis, treatment, prevention and/or prognosis of a wide range of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID No 2313; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-465566/50
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Sequence 6131 BP; 1422 A; 1665 C; 1561 G; 1483 T; 0 other;

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01-SEP-2000;
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05-SEP-2000;
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cytostatic; gene therapy; vaccine; metastasis; ds.
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17-MAR-2000;
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.5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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08-NOV-2000;
                                                                 17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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25-SEP-2000;
26-SEP-2000;
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08-SEP-2000;
                                                                                                                                                                                             08-NOV-2000;
08-NOV-2000;
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13-OCT-2000;
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21-SEP-2000;
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14-SEP-2000;
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                                                           NOV-2000;
                        2000US-0249210.
2000US-0249211.
2000US-0249212.
2000US-0249213.
2000US-0249213.
2000US-0249214.
2000US-0249218
                                                                         2000US-0249208.
2000US-0249209.
                                                                                          2000US-0246613.
2000US-0249207.
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2000US-0246477.
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2000US-0246475.
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2000US-0237040.
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2000US-0235836.
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AAQ29269

AAQ29269 standard; DNA; 6232 BP.

RESULT 12

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379 GTCCGCCTGCTGAG 392

0 Gaps

0;

EXEXEXEX X

03-MAR-1993 AAQ29269;

(first entry)

Plasmid pR14-5.3.3.1; Ca-flux assay; ss.

Human calcium channel 27980/11.

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Qy
                                                                                                   Query Match
Best Local S
Matches 14
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                             amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-
                                                                                                                             protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87594 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAKS4942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                               Sequence 6131 BP; 1422 A; 1665 C; 1561 G; 1483 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 24596; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2000;
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17-NOV-2000;
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 1 GTCCGCCTGCTGAG 14
                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NOV-2000;
                                 14;
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                                 Conservative
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2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0251869.
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2000US-0250391.
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2000US-0249300
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2000US-0249297.
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                                                 93.3%; Score 14; DB 22; 1
100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
                                 0; Mismatches
                                                               Length 6131;
                                 Indels
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AAQ37818
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                         Matches
                                                                                                                                                                                                           Best Local Similarity
AAQ37818 standard; cDNA; 7175 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (nucleotide and position in pR14-5.3.3.1 given in brackets):
1. Cytosine at position 520 (T: 3507); no change in deduced amino acid sequence. 2. Cytosine at position 775 (G: 3768); no change in deduced An sequence. 3. Cytosine at position 1617 (T:4611).
4. Adenosine at position 2360 (G: 5353). 5. deletion of 6 nucleotides at position 708 (CGGAAA; 3695-3700). 6. deletion of an Adenosine
                                                                                                                                                                                                                                                                                                                                The sequence can be inserted into a eukaryotic expression vector for use in transforming suitable host cells. Cell lines producing human neuronal calcium channel proteins can be used for screening for Ca
                                                                                                                                                                                                                                                                                                                                                                                            residue at position 1013 which leads to a stop codon at position 1028-1030. 7. at position 3240 there are a further 2199 nucleotides of the 3'UTR which are absent from pR14-5.3.3.1. (The deletion of Adenosine at position 1013 is thought to be a cloning artefact).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloned human neuronal calcium channel sub-types - useful in calcium flux assays to screen for neurone-specific calcium channel ligands
                                                                                                                                                                                                                                                                      Sequence 6232 BP; 1250 A; 1914 C; 1827 G; 1240 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                              channel ligands (agonists or antagonists). See also AAQ29259-Q29275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           containing carp skeletal muscle Ca-channel cDNA. The cDNA clone pR14-5.3.3.1 overlaps with clone p1247-14.1.1.1 (see AAQ29263). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human neuroblastoma cell line, hippocampus, frontal and temporal cortex and visual cortex cDNA banks were screened with a probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 63-77; 101pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR27649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Franz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1992.
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                                                                                                     770 TCCGCCTGCTGAGG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         following differences are observed between the two sequences
                                                                                                                                  2 TCCGCCTGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1992-333446/41.
                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rae P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91DE-4110785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= Alu_repeat
/note= "possible cloning artefact"
253..6048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "undefined"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "amino acids 358 to C-terminus
   i.e. Domains II to IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unterbeck A,
                                                                                                                                                                                                    93.3%; Score 14; DB 13; 100.0%; Pred. No. 5.9e+02;
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                                                                                                                                                                                       0;
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                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                            Length 6232;
                                                                                                                                                                                     Indels
                                                                                                                                                                                  0;
                                                                                                                                                                                  Gaps
                                                                                                                                                                                  0;
                                                                           AAQ84658
                                                                                               RESULT 14
                                                                                                                                                            B
                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                     clones to span nearly the entire length of the nucleotide sequence encoding the human alpha 1B subunit was obtained. PCR amplification of specific regions of the IMR32 cell alpha 1B mRNA yielded additional segments of the alpha 1B coding sequence. A full-length alpha 1B DNA clone was constructed by ligating portions of the partial CDNA clones (see AAQ37817, AAQ37818). Alpha 1B-1 and alpha 1B-2 are derived by alternative splicing of the alpha 1B subunit
             AAQ84658;
                                                                                                                                                            1882 TCCGCCTGCTGAGG 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A portion of one of the positive clones was used to screen an IMR32 cell cDNA library. Clones that hybridized to the basal ganglia DNA prove were used to further screen an IMR32 cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding the alpha 1B subunit was isolated by screening a human basal ganglia cDNA library with fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit-encoding cDNA.
                                                       AAQ84658 standard; DNA; 7175 BP
                                                                                                                                                                                                                                                                                                                              Sequence 7175 BP; 1415 A; 2204 C; 2162 G; 1394 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to identify overlapping clones that in turn were used to screen a human hippocampus cDNA library. In this way, a sufficient series of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 120-128; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing Tambert Eaton syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR33550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1991;
10-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human calcium channel subunit; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ37818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding specific human calcium channel sub-units - used for identifying calcium channel agonists and antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9304083-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoding the alpha 1B-2 human calcium channel subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lambert Eaton syndrome; ss.
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                  2 TCCGCCTGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ellis SB,
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0745206.
92US-0868354.
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144..6857
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                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                93.3%; Score 14; DB 14; 100.0%; Pred. No. 5.9e+02;
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                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a sufficient series of
                                                                                                                                                                                                                                                                                 Length 7175;
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0; Gaps

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1882 TCCGCCTGCTGAGG 1895

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CC library to identify overlapping clones that in turn were used to screen a human hippocampus cDNA libary. A series of clones CC to span nearly the entire length of the nt. sequence encoding the human alpha 1B subunit was obtd. Nucleic acid amplification CC of specific regions of the IMR22 cell alpha 1B mRNA yielded CC additional segments of the alpha 1B constructed by ligating portions CC of the partial cDNA clone was constructed by ligating portions CC of the partial cDNA clone was constructed by ligating portions CC of the partial cDNA clones. Nucleic acid amplification analysis of the partial cDNA clones. Nucleic acid amplification analysis CC of IMR22 cell RNA and genomic DNA using oligo primers corresp. to sequences located 5' and 3' of the stop codon of the DNA encoding the alpha 1B subunit revealed an alternatively spliced alpha CC the alpha 1B subunit revealed an alternatively spliced alpha CC to include another exon that is not present in the mRNA corresp. To the other 3' alpha 1B cDNA sequence that was initially isolated. CC to the other 3' alpha 1B cDNA sequence contg. an additional CC whereas the other form is referred to as alpha 1B-2 and is given in ANG84659/R71006. Following the sequence of the additional exon in CC alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are identical.
     Matches
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding the alpha 1B subunit was isolated by screening a human basal ganglia cDNA library with fragments of the rabbit skeletal muscle calcium channel alpha 1 subunit-encoding cDNA. A portion of one of the positive clones was used to screen an IMR32 cell cDNA library. Clones that hybridised to the basal ganglia probe were used to further screen an IMR32 cell cDNA
                                                                         Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 149-160; 285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtaining agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human calcium channel sub-unit(s) - used developing prods. for studying calcium channels, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-090900/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-1993;
05-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calcium channel subunit; antagonist; agonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lambert Eaton Syndrome; ss.
                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gillespie A,
     Conservative
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6633..7175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "identical to alpha 1B-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 144..6857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                   100.0%;
                   93.3%; Score 14; DB 16; Length 7175; 100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harpold MM,
0; Mismatches
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Q

2 TCCGCCTGCTGAGG 15 

Indels

0; Gaps

0

Query Match Best Local Similarity

Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 other;

93.3%; Score 14; DB 19; Length 7175; 100.0%; Pred. No. 5.9e+02;

Eaton Syndrome (LES) can be used as a diagnostic for the disease.

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The present sequence encodes the alpha-1B subunit of a human calcium channel. The present sequence is derived from alternative splicing of AAV42685. Calcium channels are membrane-spanning, multi-subunit proteins that allow controlled entry of calcium ions into cells. This leads to depolarisation events required for muscle contraction. The
                                       the subunits can be alternatively spliced when transcribed, giving more than one form of the protein from the same transcript, each having slightly different properties. In addition, the reactivity of the alpha 1 subunit with IgG molecules from the serum of an individual with Lambert
                                                                                                complete calcium channel, can be used in assays for the detection and characterisation of compounds that modulate the channel. The DNA encoding
                                                                                                                                                                                                                                   Claim 1; Columns 91-106; 166pp; English.
                                                                                                                                                                                                                                                                              DNA encoding human calcium channel alpha 1B sub:unit protein - useful for recombinant production of the channel for screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1989;
04-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                 recombinant subunit, when expressed with nucleic acids encoding the
                                                                                                                                                                                                                                                                                                                                              WPI; 1998-456192/39.
                                                                                                                                                                                                                                                                                                                                                                           Williams ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV42686 standard; DNA; 7175 BP.
                                                                                                                                                                                                                                                                 its modulators, and diagnosis of Lambert Eaton Syndrome
                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW63142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterisation; Lambert Eaton Syndrome; LES; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-1B subunit; human; calcium channel; assay; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human calcium channel alpha-1B-1 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                    (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                         Ellis SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89WO-US01408.
90US-0482384.
90US-0620250.
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89US-0603751
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6855..7175
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ĢΩ	Qy Db	
Search completed: Novem Job time : 64.0455 secs	y 2 b 1882	Matches
pleted 64.04	TCCGCC	14;
Search completed: November 2, 2002, 16:13:12 Job time : 64.0455 secs	Qy 2 TCCGCCTGCTGAGG 15             Db 1882 TCCGCCTGCTGAGG 1895	14; Conservative
2002		0;
2, 16:13:12		0; Mismatches
		0;
		0; Indels
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Minimum DB seq length: 0
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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15
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Copyright (c) 1993 - 2002 Compus
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SUMMARIES
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Result	Score		Length	BB	ID	Description
<u>,</u>	15	100.0	-	21	AAA38786	Human beta2 adrene
N	15	100.0	20	19	AAV30491	Canine beta-2 adre
ω	15	100.0	51	22	AAH79739	Human DNA containi
4	, 15	100.0	230	22	AAH27139	Human beta-2 adren
υı	15	100.0	1999	18	AAT93250	Beta-2 adrenalin r
6	15	100.0	2340	21	AAA38784	Human beta2 adrene
7	15	100.0	2679	19	AAV30468	Canine beta-2 adre
8	15	100.0	3451	19	AAV52614	Human beta-2-adren
9	15	100.0	3451	20	AAZ00776	Human beta 2-adren

Human manganese su	AAN81159	9	2626	89.3	13.4	45	a
	AAA38340	21	2305	89.3	13.4	44	
beta2-adren	AAX61116	20	2300	89.3	13.4	43	
polynucleot		22	2246		13.4	42	
an polynu		22	2215		13.4	41	
encoding no	AAS8512	23	1803		13.4	40	
encoding a		21	1473		13.4	9	
encoding a	AAA64425	21	1473		13.4	38	
encoding a		21	47		13.4	37	
a hu	AAA64408	21	1473		13.4	36	
2 adrenal		18	40	89.3	13.4	35	
secreted p		22	1325		13.4	34	a
		14	1008		13.4	ω U	0
္က		17	1007		13.4	32	a
_	AAT,	17	844		13.4	31	
beta-a	AAZ52371	21	746		13.4	30	
eadin		21	741		13.4	29	
adren	AAA3878	21	15		13.4	28	
DNA encoding novel		23	9896		14	27	c
EST-derived	AAH9839	22	8836		14	26	C
Human lung cell sp		22	8679		14	25	c
	×	7	8585	•	14	24	o
Homo sapiens von W		19	8575	93.3	14	23	c
Human von Willebra		21	6153	•	4	22	C
Von Willebrand fac		20	6153	93.3	4	21	C
		20	6153	•	14	20	o
		23	5548	93.3	14	19	
		23	2990	•	14	18	
melanc	ABL17701	23	2434	93.3	14	17	C
Lung cancer associ	AAF17997	21	2432	93.3	14	16	a
Drosophila melanoq	ABL17700	23	2360	93.3	14	15	
venénatu	AAF10262	21	352	93.3	14	14	
ence sequenc	AAS18444	24	3451	100.0	15	13	
beta-	AAA38339	21	3451	•	15	12	
beta	AAZ00773	20	3451	100.0	15	L1 L1	
Human beta 2-adren	AAZ00779	20	3451	100.0	15	10	

## ALIGNMENTS

	PI Li					XX V W O		XX						xx			××		ID AA	AAA38786	777077
WPI; 2000-400107/34.	Liggett SB;	(UYCI-) UNIV CINCINNATI.	25-NOV-1998; 98US-0109886.	24-NOV-1999; 99WO-US27963.	02-JUN-2000.	W0200031307-A1.	Homo sapiens.	affere-specific origonucteoride probe; ss.	anaphylaxis; chronic obstructive pulmonary disease;	obesity; diabetes; vascular disease; premature labour;	congestive heart failure; ischemic heart disease; arrhythmia;	chromosome 5q31(12); disease predisposition; asthma; hypertension;	<pre>Human; adrenergic receptor; beta2 adrenergic receptor;</pre>		Human beta2 adrenergic receptor beta2AR C allele-specific probe.	U5-UCT-2000 (Ilrst entry)		AAA38786;	AAA38786 standard; DNA; 15 BP.	80E2 1 838786	
										migraine;	thmia;	pertension;	beta2AR;	,	ic probe.						

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AAV30491
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an injurious it the susceptibility of an injurious in the susceptibility of an injurious contents.
                                                                                                                     Canine beta 2 and beta 3 adrenergic receptors and coding sequences useful for identifying specific ligands and (ant)agonists to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
beta-2 receptor can be used in comparative
                Primers AAV30491-V30510 were used for sequencing the coding region of the canine beta 2-adrenergic receptor (RA-Ca-b2) gene (AAV30468). The
                                                                     Claim 17; Page 55; 79pp;
                                                                                                                                                                                                              Drumare MF, Lenzen G,
                                                                                                                                                                                                                                                                                                                                                        02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                         W09735973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridisation; ligand; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine beta-2 adrenergic receptor sense primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 1 A; 6 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alleles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for the C allele of which is located on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension -
                                                                                                        specific treatments for
                                                                                                                                                                             WPI; 1998-032136/03.
                                                                                                                                                                                                                                                 (VETI-) VETIGEN.
                                                                                                                                                                                                                                                                                    26-MAR-1996;
                                                                                                                                                                                                                                                                                                                     26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV30491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in lividual to these diseases and determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Page 11; 56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-adrenergic receptor; brown adipose tissue; probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ent sequence is an allele-specific oligonucleotide probe callele of the human beta2 adrenergic receptor (beta2k9) gene, located on chromosome 5431 (12). The gene has two different and it has been shown that the presence of two copies of the T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                    96FR-0003730
                                                                                                                                                                                                                                                                                                                     97WO-FR00537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                        obesity in
                                                                                                                                                                                                                Pietri-Rouxel F,
                                                                     French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 21;
Pred. No. 1.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                              Strosberg AD
 structure-function studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                and activity of proteins related to angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phosphoglycerate kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. for differential screening of ligands specific for RA-Ca-b3 (AAW44933).
                                                                                                                                           proteins have potential immunosuppressive, immunostimulatory, antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostati antilieukemic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression
                                                                                                                                                                                                                                      angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphospha (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phosphoglycerate kinase. 1
                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antisclerotic; antidiabetic; antiinflammatory;
antileukemic; neuroprotective; antimicrobial; gene therapy; va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           major histocompatibility complex Class I histocompatibility an
phosphoglycerate kinase; immunosuppressive; immunostimulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DNA containing single nucleotide polymorphism SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH79739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH79739 standard; DNA; 51
               rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
                                diseases with a genetic component, such as autoimmune diseases (e.g.
                                                                                                                                                                                                                      nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
                                                                                                                                                                                                                                                                                          The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 162; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-418297/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4-hydroxybutyrate; dehydrogenase; protein therapy;
adenosine triphosphate-dependent RNA helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; single nucleotide polymorphism; SNP; angiopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 100 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 BP; 2 A; 8 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0472688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complex Class I histocompatibility antigen; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 Ţ;
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                                                                                                                                                                                                                                                                          dehydrogenase, adenosine triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA-Ca-b2 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                   cytostatic,
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erytheromatosus and Grave's disease),

inflammation,

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Best Local Similarity
              Query Match
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                                                                                               modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBBs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP interaction or mRNA functionality; or RBPs that interact with the compounds identified using the gene fragments are potentially useful for therapeutic regulation of gene expression, such as in cases of neurodegeneration, stroke; cardiovascular disease, hypertension, cancer.
                                      Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;
                                                                                                                                                                                                    of mRNA from the nucleus to the cytoplasm, mRNA stabilisation. Therefore translational efficiency, and the sequestration of some mRNAs. Therefore
                                                                                                                                                                                                                               Sequences AAH27132 - AAH27151 represent human gene untranslated regions where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity. RBPs mediate the processing of pre-mRNA, the transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration; stroke; cardiovascular disease; hypertension; cancer; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH27139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be used to alter phenotypic traits such as longevity, appearance,
                                                           viral infection. The present sequence is one of gene fragments of the invention, isolated from the human beta-2 adrenergic receptor gene.
                                                                                                                                                                                                                                                                                    Claim 1; Page 28; 33pp; English.
                                                                                                                                                                                                                                                                                                                neurodegeneration
                                                                                                                                                                                                                                                                                                                         New nucleic acids that bind RNA-binding proteins or regulate mRNA function, useful for therapeutic gene regulation, such as in cases
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-335904/35
                                                                                                                                                                                                                                                                                                                                                                                           Giordano A,
                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000; 2000WO-US30888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta-2 adrenergic receptor UTR region with RBP binding ability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                                     (MESS-) MESSAGE PHARM INC
                                                                                        inflammation; metabolic disorders (obesity and diabetes) and bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                           Xavier AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0437458
 100.0%;
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Pred. No. 1.2e+02;
            Score 15;
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             DB 22;
          Length 230;
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                                                                                                    RESULT 6
AAA38784
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                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujii K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09735963-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT93250;
                                                              AAA38784;
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This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 125I-cyanopindrol. The protein can be used in screening for agonists and antagonists, which are useful in researching asthmatic diseases.
Human beta2 adrenergic receptor beta2AR gene.
                                         05-OCT-2000 (first entry)
                                                                                                                                      AAA38784 standard; DNA; 2340 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 27-30; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agonists and antagonists and researching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel beta-2 adrenalin receptor sub-type - useful for screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-489627/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
asthmatic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-2 adrenalin receptor subtype coding sequence
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                                                                                                                                                                                                                                                        136 GTCCGCCCGCTGAGG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawashima H,
                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                           Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nomura A,
                                                                                                                                                                                                                                                                                                                                                                           1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                            DB 18; Length 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthmatic diseases
                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                            RESULT
Χij
                              AAV30468
                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                      influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and
                                                                                                                                                                                                                                                                                                                                                 adrenergic receptor (beta2AR) gene, which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the Tallele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to
                                                                                            1534 GTCCGCCCGCTGAGG 1548
             AAV30468 standard; cDNA to mRNA; 2679 BP
                                                                                                                                                                                                                         Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine;
                                                                                                                                                                                                                                                            determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a fragment of the C allele of the human beta2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Figure 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liggett SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCI-) UNIV CINCINNATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypertension -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaphylaxis; chronic obstructive pulmonary disease; ds.
                                                                                                                                                                           Local Similarity
                                                                                                                         1 GTCCGCCCGCTGAGG 15
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0109886
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1588..2340
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/product= "beta2 adrenergic receptor"
/note= "no stop codon given at 3' end of sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= 5'_leader_cistron
replace(1541,T)
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                                                                                                                                                                        100.0%;
                                                                                                                                                            0;
                                                                                                                                                                         Score 15; DB 21;
Pred. No. 1.2e+02;
                                                                                                                                                            Mismatches
                                                                                                                                                                                         DB 21;
                                                                                                                                                                                       Length 2340;
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                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                           This sequence represent the coding region of the canine beta 2-adrenergic receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library constructed from polyA+ RNA purified from dog brown adipose tissue cells. The probe was a 600 bp fragment of the coding region of the human beta-3 adrenergic receptor covering the region from the initiation codon to transmembrane domain 5 (TM5). The full length insert was cloned into M13 for sequencing using primers AAV30491-V30510. The sequence can then be expressed e.g. in a mammalian cell, by subcloning into an expression vector such as pCDNA3. The beta-2 receptor can be used in comparative structure-function studies, e.g. for differential screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine beta 2 and beta 3 adrenergic receptors and coding sequences - useful for identifying specific ligands and (ant)agonists to develop specific treatments for obesity in dogs
                                                      Human beta-2-adrenergic receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                    Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T; 0 other;
              polymorphism;
                        Beta-2-adrenergic receptor; human; asthma; beta-agonist;
                                                                                        21-DEC-1998
                                                                                                                                                    AAV52614 standard; cDNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                 of ligands specific for RA-Ca-b2 or RA-Ca-b3 (AAW44933).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW44932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine; beta-adrenergic receptor; brown adipose tissue; probe; human; hybridisation; ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine beta-2 adrenergic receptor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV30468;
                                                                                                                                                                                                                              122 GTCCGCCCGCTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (VETI-) VETIGEN
                                                                                                                                                                                                                                                           1 GTCCGCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                          Conservative
                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "beta-2 adrenergic receptor"
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                                                                                                                                                                                                                                136
                                                                                                                                                                                                                                                                                                        100.0%; Score 15; DB 19; Length 2679; 100.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                       Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strosberg AD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or perferably comprises amplifying at residue 16, and optionally also options to comprise the sequence analysis. The includes the sequence analysis. The inventor of these portions of these portions of the parameter of the second alleles of the beta 2-adrenergic receptor gene, and (b) classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor gene alleles may be identified by any known method e.g. denaturing gel electrophoresis or PCR amplification (see also AAV52615-17). Identification preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also by automated sequence analysis). The invention identifies a known in the heat 2-adreners in the protection of these portions (e.g. by automated sequence analysis). The invention identifies a known in the heat 2-adreners in the protection of the protection is a known in the protection of the protection is a known in the protection of the protection is a known in the protection of the protection is a known in the protection of the protection is a known in the protection of the protection is a known in the protection in the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protection is a protection of the protection in the protec
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Human beta 2-adrenergic receptor DNA variant 3.
                                                                                                                                                                                                                                                                                     1534 GTCCGCCCGCTGAGG 1548
                                                          07-OCT-1999
                                                                                                         AAZ00776;
                                                                                                                                                   AAZ00776 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphism in the beta 2-adrenergic receptor gene as being linked to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and individuals homozygous for Arg16 are more susceptible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patients homozygous for allele encoding Arg at position 16 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA sequence codes for human beta-2-adrenergic receptor (see AAW/5777) having an arginine residue at position 16. A novel method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 33-35; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-506372/43.
P-PSDB; AAW75777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boushey H,
Martin RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                     1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chinchilli VM, Drazen JM,
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0811441
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1633
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1588..2829
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ь
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                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15;
                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.1e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19; Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post tranmatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                               and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                                             predicting a change in weight, using body mass index, can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 2a; 27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-479048/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(1666,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wild type amino acid sequence from an Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue to Arg residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residue to Gln residue"
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Query Match Best Local Similarity

100.0%;

Score 15; Pred. No.

DB 20; 1.1e+02;

Length 3451;

Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;

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RESULT 10
AAZOO779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
           This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
   for abnormal blood
                                                                                        Claim 7; Fig
                                                                                                                      determining an individuals haplotype
                                                                                                                                    Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                   Hoehe M,
                                                                                                                                                                                                                                                               30-DEC-1997;
                                                                                                                                                                                                                                                                                          30-DEC-1998;
                                                                                                                                                                                                                                                                                                                       29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                     W09937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS
                                                                                                                                                                                                                             (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta 2-adrenergic receptor DNA variant 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ00779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ00779 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1534 GTCCGCCCGCTGAGG 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                     1999-479048/40.
                                                                                                                                                                                                Koepke K, Timmermann B;
                                                                                          2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                            97DE-1058401.
                                                                                                                                                                                                                                                                                          98WO-DE03818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1666,c)
/*tag===c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace(1633,a)
                                                                                      27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(1568,t)
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
 pressure and other cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                       "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an {\tt Gly}
                                                                                                                                                                                                                                                                                                                                                                                residue to Gln residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ت</u>
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                     AAZ00774" mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1534 GTCCGCCCGCTGAGG 1548
                                                                                                                              AAZ00774" mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ00773 standard; DNA; 3451 BP
                                                                                                                                                                                                        AAZ00774* mutation
                                                                                                                                                                                                                                                                               AAZ00774" mutation
                                                                                                                                                                                                                                                                                                                                                          AAZ00774" mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta 2-adrenergic receptor wild type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ00773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3451 BP; 789 A; 873 C; 897 G; 892 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anorexia nervosa and bulimia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attention deficit disorder with hyperactivity, eating disorders, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocardial infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determined include neuropsychiatric disease, such as depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOCGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                orexia nervosa and bulimia, or post-traumatic stress disorder. Dise
the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                           /note= "This nucleotide differs from the wild type
sequence in the sequence represented in
               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(159,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                            /*tag=
                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 15; DB 20;
                                                                                                                                                                                                                                                                                                                                                                          "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                    "This nucleotide differs from the wild
                                                                                                                                                                                                                        "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                   "This nucleotide differs from the wild type
sequence in the sequence represented in
                                                                    sequence in the sequence represented
                                                                                                                                                                                                                                                                                                 sequence in the sequence represented
                                                     replace(1221,t)
                                                                                                                            replace(1120,c)
                                                                                                                                                                                                        replace(934,a)
                                                                                                                                                                                                                                                                               replace(565,a)
                                                                                                                                                                                                                                                                                                                                                      replace(245,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                        d type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anxiety,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as
                                                        This invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                             AA200774" mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation
                                                                                     Disclosure; Fig 2a; 27pp; German.
                                                                                                                 Human beta2-adrenergic receptor gene variants, useful for
determining an individuals haplotype
                                                                                                                                                             WPI; 1999-479048/40.
                                                                                                                                                                                          Hoehe M,
                                                                                                                                                                                                                                                    30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                         W09937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ00774" mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ00774" mutation
for abnormal blood pressure and other cardiovascular diseases,
                                                                                                                                                                                                                       (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                30-DEC-1998;
                                                                                                                                                                                                                                                                                                             29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ00774" mutation
                                                                                                                                                                                         Koepke K,
                                                                                                                                                                                                                                                    97DE-1058401.
                                                                                                                                                                                                                                                                                98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(2110,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "This nucleotide differs from the wild type
sequence in the sequence represented in
    replace(2078,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1839,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(1666,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(1633,g)
/*tag= i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1568,c)
                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                          Timmermann B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "This mutation results in a change in the corresponding wild type amino acid sequence from a Thr residue to Ile residue"
                                                                                                                                                                                                                                                                                                                                                                                  "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "This nucleotide differs from the wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "This mutation results in a change in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "This nucleotide differs from the wild type
in the variant nucleotide sequences repres
in AAZ00774 and AAZ00779"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "This mutation results in a change in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "This mutation results in a change in the corresponding wild type amino acid sequence from an Arg residue to Cys residue in the
                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponding wild type amino acid sequence from an Arg residue to Gly residue in the variant sequences represented in AR200774, AA200776, AA200777, AAX00779 and AAZ00780"
                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence in the sequence represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variant sequences represented in AAZ00774, AAZ00776, AAZ00779"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       corresponding wild type amino acid sequence from a Gln residue to Glu residue in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variant sequences represented in AAZ00774, AAZ00775, AAZ00777, AAZ00778 and AAZ00780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(2640,c)
                                                                                                                                                                                                                                                                                                                                                                                                                              replace(2826,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in AAZ00774
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AAA38339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta
receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1534 GTCCGCCCGCTGAGG 1548
                                                                                 The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This
                                                                aldosterone synthase, endothelin receptor type A and beta-adrenergic
                                                                                                                                                                                       Disclosure; Page 123-124; 126pp; English.
                                                                                                                                                                                                                               polymorphic pattern comprising polymorphic positions within genes
encoding specific proteins, with reference polymorphic pattern -
                                                                                                                                                                                                                                                                      Assessing cardiovascular status in humans involves comparing test
                                                                                                                                                                                                                                                                                                                                                        Norberg LT, Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                               (EURO-) EURONA MEDICAL AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0200022166-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stroke; prognosis; drug screening; treatment outcome; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymorphism; polymorphic marker; cardiovascular dise
myocardial infarction; unstable angina; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-adrenergic receptor-2 gene; regulatory region; polymorphism; polymorphic marker; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta-adrenergic receptor-2 gene regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA38339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA38339 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents the wild type human beta 2-adrenergic receptor gene which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myocardial infarction and stroke. Other conditions that can be determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                 2000-318010/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        9808-0104302
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0104286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-IB01678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                          Lindstrom PHR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1e+02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                          Jonsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
      polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 13
AAS18444
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                                                                                                                                                                                                                                                                                                                               Human; beta2-adrenergic receptor; beta2AR polymorphism; asthma; chromosome 5q31-32; migraine; congestive heart failure; hypertension; ischaemic heart disease; chronic obstructive pulmonary disease; COPD; obesity; diabetes mellitus; premature labour; vasotropic; cardiant; antiarrhythmic; antiasthmatic; antidiabetic; tocolytic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost trials. The present sequence represents the human beta-adrenergic receptor-2 gene regulatory region (GenBank M15169, J02728, M16106). The polymorphic sites identified are 934A/G, 987C/G, 1006A/G, 1120C/G, 1221C/T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen. Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular individual cardiovascular pattient. It also provides the ability to
                                                                                                                                                                    variation
                                       variation
                                                                                                    variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1534 GTCCGCCGCTGAGG 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial
                                                                                                                                                                                                                                                     Ϋ́
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference sequence for human beta2AR gene showing polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS18444 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular
                                                                                                                                                                                                                               cariation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1541C/T and 1568C/T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTCCGCCCGCTGAGG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                     replace
                                                                                                    replace
                                                                                                                                                                 replace
                                                                                                                        /note=
                                                                                                                                                                                   /note=
                                                                                                                                                                                                                               replace
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                           /note= "Polymorphic site 3 (PS3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                               "Polymorphic site 1 (PS1)"
e (879, A)
"Polymorphic site 4 (PS4)"
                                                                                                                        "Polymorphic site 2 (PS2)"
                                                                                                                                                                                                                             (565,
                                                                                                    (934,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15; DB 21; L
; Pred. No. 1.1e+02;
... wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unstable angina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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The present invention relates to polymorphisms and haplotypes of Ct the human beta2-adrenergic receptor (beta2-R) gene located on Ct the human beta2-adrenergic receptor (beta2-R) gene located on Ct chromosome 5q31-32, and methods for haplotyping and/or genotyping the Ct chromosome 5q31-32, and methods for haplotyping and/or genotyping the Ct beta2AR gene in an individual. The methods of the invention make use of allele-specific oligonucleotides (ASOS) as probes and primers for callele-specific oligonucleotides (ASOS) as probes and primers for detecting the beta2AR gene polymorphisms. The beta2AR gene polymorphisms are useful in studying the expression and biological function of beta2AR, and for developing drugs targeting this receptor. They are also useful can developing drugs targeting this receptor. They are also useful corression or function of beta2AR such as congestive heart failure, as rhythmia, ischaemic heart disease, hypertension, migraine, asthma, chromic obstructive pulmonary disease (COPD), obesity, diabetes and premature labour. The method is useful for determining the frequency of a beta2AR genotype or haplotype in a population. The present sequence
                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                     New isolated beta 2-adrenergic receptor polynucleotide, useful for studying expression and biological function of receptor and for
                                                                                                                                                                                                                                                                                                                        developing drugs targeting receptor, comprises polymorphism of adenosine at PS2 and thymine at PS5 - \,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-061968/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variation
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                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAU10763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stack CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-APR-2000; 2000WO-US10125
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                                            represents a reference sequence for the human beta2AR gene which shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liggett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCI-) UNIV CINCINNATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-APR-2000; 2000WO-US10125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drysdale CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Polymorphic site 7 (PS7)"
replace (1568, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Polymorphic replace (1541, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace (1221,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product= "Beta2AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L588..2829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Polymorphic site 10 (PS10)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (2110, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stephens JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site 6 (PS6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site 11 (PS11)"
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Sequence 3451 BP;

790 A; 873 C;

895

G; 893 T; 0 other

the polymorphisms in the gene.

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RESULT 14
AAF10262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                              engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                          adapt to changes in culture conditions, environmental stress, spore
                                                                                                                                                                                                                                                                                                                                                                   identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 86; Page 1393; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusarium venenatum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1534 GTCCGCCCGCTGAGG 1548
                                            AAF14879
                                                                                                                                                                                                                                                                                                         morphogenesis, recombination, metabolic or catabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for monitoring differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-594572/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-2000; 2000WO-US07781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     discovered, possible functions of unknown open reading frames can be
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14879 to AAF15337 represents ESTs from Trichoderma reesei, which are specifically claimed in the present invention.
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                                                                                                                                                                                     cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                   Sequence 2360 BP; 555 A; 620 C; 613 G; 572 T; 0 other;
                                                                                                                                                          sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                 useful in developmental biology and in elucidating cell signalling
                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4573; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                  genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more
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                                           Local Similarity
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1 GTCCGCCCGCTGAG 14
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                            Conservative
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Search completed: November Job time: 64.0455 secs

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Maximum DB seq length: 200000000
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-456-2008-17
US-08-311-363-14
US-08-311-363-12
US-08-311-363-12
US-08-311-363-12
US-08-456-2068-11
US-08-456-208-11
US-08-193-078B-8
US-08-193-078B-8
US-08-1949-386-8
US-08-949-386-8
US-08-949-386-8
US-08-949-709A-8
US-08-945-562-8
US-08-945-562-8
US-08-945-562-7
US-08-945-563-7
US-08-945-563-3
US-09-268-163-5
US-09-268-163-5
US-09-268-163-5
US-09-268-163-3
US-08-060-9258-12
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

17:

TELEX:

REGISTRATION NUMBER: 33,141
REFRENCE/DOCKET NUMBER: Bas
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844

Bayer 8398.3-KGB

RESULT 1 US-08-456-200B-17 Sequence 17, Application US/08456200B Sequence 17, Application US/08456200B Retent No. 6229000 GENERAL INFORMATION: THE STATE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND TITLE OF INVENTION: THEIR USE NUMBER OU SEQUENCES: 17 CORRESPONDENCE ADDRESS: ADDRESSE: SPRING HORN KRAMER & WOODS STREET: 660 White Plains Road CITY: Tarrytown CITY: Tarrytown STATE: New York COUNTRY: U.S.A. ZIP: 10591-5144 COMPUTER: New York COUNTRY: U.S.A. ZIP: 10591-5144 COMPUTER: NEC POWERMATE SX/20 ODERATING SYSTEM DOS SOFTWARE: WOIDSERTED SOS SOFTWARE: WOIDSERTED SOS SOFTWARE: WOIDSERTED SOS COMPUTER: NEC POWERMATE SX/20 ODERATION NUMBER: US/08/456,200B FILING DATE: 31-MAY-1995 CLASSIFICATION NUMBER: 08/094,712 FILING DATE: 19-JUL-1993 PRIOR APPLICATION NUMBER: 08/094,712 FILING DATE: 19-JUL-1993 PRIOR APPLICATION NUMBER: 08/094,712 FILING DATE: 19-JUL-1993 PRIOR APPLICATION NUMBER: 08/064,778 FILING DATE: 19-MAY-1993 PRIOR APPLICATION NUMBER: 08/064,778 FILING DATE: 19-MAY-1993 PRIOR APPLICATION NUMBER: DE 41 10 785 FILING DATE: 19-MAY-1993 PRIOR APPLICATION NUMBER: DE 41 10 785 FILING DATE: 04-APR-1991 ATTORNEY/AGENT INFORMATION: NUMBER: WOIL OF APR-1991 ATTORNEY/AGENT INFORMATION: NUMBER: WOIL OF APR-1991 ATTORNEY/AGENT INFORMATION: WIMBER: WOIL OF APR-1991 ATTORNEY AGENT INFORMATION: WIMBER: WOIL OF APR-1991 ATTORNEY AFTORNEY APR-1993	28 13.4 89.3 36 1 US-08-291-932A-565 29 13.4 89.3 36 1 US-08-291-932A-754 30 13.4 89.3 36 2 US-08-292-620A-1339 31 13.4 89.3 36 2 US-08-292-620A-1339 32 13.4 89.3 36 3 US-09-071-845-1386 32 13.4 89.3 36 3 US-09-071-845-1386 34 13.4 89.3 308 2 US-08-673-190A-4 c 36 13.4 89.3 308 2 US-08-673-190A-4 c 36 13.4 89.3 5904 1 US-09-286-529-18 39 13.4 89.3 5904 1 US-09-28-529-18 40 13.4 89.3 5904 1 US-08-455-543A-3 41 13.4 89.3 5904 2 US-08-13-0728-3 41 13.4 89.3 5904 2 US-08-13-305-03 42 13.4 89.3 5904 2 US-08-13-365-6 43 13.4 89.3 5904 2 US-08-13-86-3 44 13.4 89.3 6575 3 US-08-949-386-3 45 13.4 89.3 6575 4 US-08-947-799A-3 45 13.4 89.3 6575 4 US-08-947-799A-3
	Sequence 565, App Sequence 133, App Sequence 1386, Ap Sequence 1386, Ap Sequence 1386, Ap Sequence 18, Appli Sequence 4, Appli Sequence 6, Appli Sequence 3, Appli

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US-08-311-363-14
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                                                                                                                          Matches
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Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                          TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2470 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
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                                                           1739 TCCGCCTGCTGAGG 1752
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TELECOMMUNICATION INFORMATION:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                     Local Similarity
                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 1..2469
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                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fitch, Even, Tabin & Flannery STREET: 135 S. LaSalle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Single
                                                                                         2 TCCGCCTGCTGAGG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TCCGCCTGCTGAGG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
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Feldman, Da
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                                                                                                                        Conservative
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Ellis, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         19910815
                                                                                                                                                                                                                                                                                unknown
                                                                                                                                  100.0%;
                                                                                                                                    93.3%; Score 14; DB 1; Length 2470; 100.0%; Pred. No. 77;
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                                                                                                                       Mismatches
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US-07-745-206A-12
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                                                                                                                                                                                          Sequence 12, Application US/07745206A Patent No. 5429921
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APPLICANT: Harpold
APPLICANT: Ellis,
APPLICANT: William
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.3%; Score 14; DB 2; Length 2470; Best Local Similarity 100.0%; Pred. No. 77;
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INFORMATIC: FOR SEQ ID NO: 14:
                                                                                     APPLICANT:
APPLICANT:
              APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                     APPLICANT: Harpold, Michael APPLICANT: Ellis, Steven
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REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: unknown
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ADDRESSEE:
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                                                                                                                      Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Ellis, Steven
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                                                                                                     McCue, Ann
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Fitch, Even, Tabin & Flannery
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US-08-311-363-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08311363 Patent No. 5876958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
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CITY: Chicago
CITY: Illinois
T.S.A.
                                                                                                                                                                                                                                                                                                   APPLICANT: Brenner, Robert TITLE OF INVENTION: Human TITLE OF INVENTION: Method
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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LOCATION: .3392, 3396..3488, 3495..3539, 3543..3581, 3585

LOCATION: ..3587, 3396..3626, 3630..3689, 3693..3737, 3744

LOCATION: ..3746, 3750..4823, 4827..4841, 4845..5006, 5010

LOCATION: ..5096, 5100..5306, 5310..5366, 5370..5465)
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REFERENCE/DOCKET NUMBER:
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FILING DATE:
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                         STATE:
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                                                                                                                                                                                     California
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                                                                                                                                                                                                                           1660 Union Street
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Feldman, Daniel
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Ellis, Steven
                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 14; Conservative
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APPLICANT: Franz, Jurgen; Weingartner, Bernhard;
APPLICANT: Unterbeck, Axel; Rae, Peter
TITLE OF INVENTION: TISSUE-SPECIFIC (UMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
TITLE OF INVENTION: THEIR USE
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REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5467 base pairs
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                                                    APPLICATION NUMBER:
FILING DATE: 26-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/094,712
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 105
                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 31-MA
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                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 93.3%; Score 14; DB 2; Length 5467; Local Similarity 100.0%; Pred. No. 78;
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                     FILING DATE:
                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.1
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                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                        10591-5144
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tarrytown
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SPRUNG HORN KRAMER & WOODS 660 White Plains Road
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..3392, 3396..3488, 3495..359, 3543..3561, 3585
..3587, 3591..3626, 3630..3689, 3693..3773, 3744
..3746, 3750..4823, 4827..4841, 4845..5006, 5010
..5096, 5100..5306, 5310..5366, 5370..5465)
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                                                                                                                                       19-JUL-1993
                     19-MAY-1993
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                                                                              26-MAR-1992
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                                                                                               07/858,278
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                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
                                                                                                                                                          FILING DATE: April 10, 1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                           APPLICATION NUMBER: 08/223
FILING DATE: APRIL 4, 1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
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                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                                                                     FILING DATE:
                                                                                                                           FILING DATE: 15-AUG-1991
                                                                                                                                          APPLICATION NUMBER: US 07/745,206
                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: May 3:
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STATE: California
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                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Brown, Martin, Haller & McClain 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, Mark
Feldman, Daniel
McCue, Ann
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Ellis, Steven
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                    20-FEB-1990
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                                                                                     US 07/620,250
                                                                                                                                                                                                07/868,354
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                                                                                                                                                                                                                                                                                                                                                                                                                               ; Patent No. 5846757
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LENGTH: 7175 base pairs
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                                                                                                                                                                                                                                                                                               APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN OF TITLE OF INVENTION: METHODS
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APPLICATION NUMBER: WO PCT/US89/01408
PRIOR APPLICATION DATA:
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LOCATION:
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LOCATION:
               APPLICATION NUMBER: US/O FILING DATE: 07-FEB-1994 CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: 6362-52517
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REGISTRATION NUMBER: 33,779
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                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                 CITY:
                                                                                                                                                                                                                               ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN STREET: 1660 UNION STREET
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Local Similarity 100.0%; Pred. No. 78;
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Feldman, Daniel
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Ellis, Steven
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1..143
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6855..7175
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144..6857
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 Mismatches

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RESULT 9
US-08-223-305C-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08223305C
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                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
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               APPLICATION NUMBER: 07/868,354 FILING DATE: April 10, 1992 PRIOR APPLICATION DATA:
                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                              ADDRESSEE: Brown, ADDRESSEE: 1660 Union Street
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7175 base pairs TYPE: nucleic acid STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 63
                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie L. REGISTRATION NUMBER: 33,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TCCGCCTGCTGAGG 15
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                                                                                                                                                                                                                   92101-2926
                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                  USA
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Feldman, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Ellis, Steven
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144..6857
                                                                                                                                                           IBM Compatible
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1..143
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                                                                                                                                                                                                                                                                                                 Brown, Martin, Haller & McClain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 14; DB 100.0%; Pred. No. 78;
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us 07/745,206
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                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08149097D Patent No. 5874236
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Best Local Similarity
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                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      1882 TCCGCCTGCTGAGG 1895
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                          APPLICANT: Brenner, Robert TITLE OF INVENTION: HUMAN CONTILLE OF INVENTION: METHODS MUMBER OF SEQUENCES: 40
                                                                                                                             CORRESPONDENCE ADDRESS
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LENGTH: 7175 base pairs
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION UNBER: US 07/620,250
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LOCATION:
                                   COUNTRY: USA
ZIP: 92101-2926
                                                                 STATE:
                                                                                               STREET:
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REFERENCE/DOCKET NUMBER: 52516
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                                                                                San Diego
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                                                               California
                                                                                            E: Brown, Martin, Haller & McClain
1660 Union Street
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Williams, Mark
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                                                                                                                                                                         HUMAN CALCIUM CHANNEL COMPOSITIONS AND
                                                                                                                                                             METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Score 14; DB 2; Length 7175; 100.0%; Pred. No. 78;
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В
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                                                                    Matches
                                                                                                   Query Match
                                                                                                                                                                  FEATURE:
NAME/KEY:
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SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
1882 TCCGCCTGCTGAGG 1895
                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
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PRIOR APPLICATION NUMBER: US 07/482,384
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APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                   Local Similarity
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                               2 TCCGCCTGCTGAGG 15
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                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                   Conservative
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                                                                               93.3%; Score 14; DB 2; Length 7175; 100.0%; Pred. No. 78;
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                                                                 0; Mismatches
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                                                                 Indels
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RESULT 11 US-08-949-386-8

; Sequence 8, plication US/08450562
; Patent No. 6096514

RESULT 12 US-08-450-562-

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                                                             Matches
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                                                                                            Query Match
                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 238-0062 INFORMATION FOR SEQ ID NO:
1882 TCCGCCTGCTGAGG 1895
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                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                       NAME/KEY:
                                                                                                                                                                                     NAME/KEY:
LOCATION:
                             2 TCCGCCTGCTGAGG 15
                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Brown, Martin, Haller & McClain STREET: 1660 Union Street
                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 5-NOV-1993
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                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                           Conservative
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Ellis, Steven
                                                                                                                                     3'UTR
6855..7175
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                                                                                                                                                                                       1..143
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                                                                          93.3%; Score 14; DB 3; 100.0%; Pred. No. 78;
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 Mismatches

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                                                                                            Length 7175;
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GENERAL INFORMATION:
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                                                                PRIOR APPLICATION DATA:
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                PRIOR APPLICATION DATA:
                                                                                                                    PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 07/91
FILING DATE: 13-JULY-1992
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APPLICATION NUMBER: 08/105,536
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APPLICATION NUMBER: 08/311,363
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APPLICATION NUMBER: 08/404,950
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                                 APPLICATION NUMBER: 07/603,751 FILING DATE: 08-NOV-1990
                                                                                                                                     APPLICATION NUMBER: 07/745,206 FILING DATE: 15-AUG-1991
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APPLICATION NUMBER:
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APPLICATION NUMBER: 08/3
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Gillespie, Alison
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                             07/868,354
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07/482,384
                                                                                                   07/620,250
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RESULT 13
US-08-984-709A-8
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US-08-450-562-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08984709A Patent No. 6320032
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                              ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
                                                                                                                                SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williams, Mark E. APPLICANT: Stauderman, Kenneth APPLICANT: Harpold, Michael M. TITLE OF INVENTION: HUMAN CALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1882 TCCGCCTGCTGAGG 1895
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NAME/KEY:
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LENGTH: 7175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
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FILING DATE: 04-APR-
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 02-DEC-1997
                                                                                                                                                                                       COMPUTER:
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                                                                                   CLASSIFICATION:
                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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(619) 238-000
                                                                                                                                                                                                                                                                                                       E: Heller Ehrman White & McAuliffe 4250 Executive Square, Suite 700
                                                                                                                                                                                                                                                         SD
                                                                                                                                                                                                                                                                                                                                                                                                                           Stauderman, Kenneth A.
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                                                                                                                                                 FastSEQ Version 1.5
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                                                                                                                     US/08/984,709A
                24735-9815 (formerly 6362-9815)
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TELEPHONE:

: (619) 450-8400 (619) 587-5360

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; LOCATION: 146..6856
US-09-268-163-7
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US-08-984-709A-8
                                                                                                                                                                          RESULT 15
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                                                                                                                     Sequence 1, Application US/08713118 Patent No. 6040436
                                                                                                                                                                                                                                                                                               Matches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lipscombe, Diane
APPLICANT: Schorge, Stephanie
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THERBOF
TILE REFERENCE: B1055/7000
CURRENT FAPLICATION NUMBER: US/09/268,163B
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 60/077,901
EARLIER FILING DATE: 1998-03-13
EARLIER FILING DATE: 1998-03-13
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                                                                                                   GENERAL INFORMATION:
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       APPLICANT: Franco, Rodrigo
APPLICANT: Sun Chen, Ai Ru
APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1882 TCCGCCTGCTGAGG 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CENGTH:
                                                                                                                                                                                                                          1884 TCCGCCTGCTGAGG 1897
NUMBER OF SEQUENCES:
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ative 0;
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                                                                                                                                                                                                                                                                                              Mismatches
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Search completed: November Job time: 16.9091 secs
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                                                                                                                                      Matches
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                                                                1830 TCCGCCTGCTGAGG 1843
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: ACC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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Local Similarity 100.0%; Pred. No. 78;
les 14; Conservative 0; Mismatches 0; Indels
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mata, Elizabeth REGISTRATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 16-SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                2002, 16:50:54
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                  110
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CNS04KMI
  BM309817
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375.200 Million cell updates/sec
                    AA015272 mh30g12,r
BE419553 WWS014 E1
BE770021 CM1-FT005
AA763593 vp06a08.r
AI210517 i7g01a1.r
                                                                                                                           AV647785 AV647785
AQ759327 HS 3116 A
B1907636 603065545
BJ001358 BJ001358
BG284879 602409113
AL295011 Tetraodon
                                                                               AL553611 AL553611
AL270645 Tetraodon
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                                                                                                     BI767868 603060993
BI915042 603177231
BG366430 HVSME1000
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COMMENT
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AV647785
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                                                                                                                                                                                                                                                             Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
                                                                                                                         Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                     Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                           by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
                                                                                                                                                  Fax: 86-21-50801922
                                                                                                                                                          201203, P. R. China
Tel: 86-21-50801919(ex.45)
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                                                                                                                                                                                                                                                                                                                                     Mammalia;
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(bases 1 to 427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
        /lab_host="SOLR"
/note="Vector: pBluescript sk(-);    Site_1: EcoRI;    Site_2:
                                                       /clone_lib="GLC"
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                                                                   /clone="GLCBCA03"
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BE499548 WHE9961_B
AL491062 T. brucei
Bi140168 Ir1_50_A0
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AUZ41418 AUZ41418
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AW621109 707003F05
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AL143288 Anopheles
AL190797 Tetraodon
BF038061 601461843
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BI907636
BI907636.1 GI:16170473
                                     603065545F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214802 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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1 (bases 1 to 580)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                             BI907636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC end Web Server: http://www.htsc.washington.edu
Plate: 3116 row: A column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Plate=3116 Col=5 Row=A"
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTCCGCCTGCTGAGG 15
                                         Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                            Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                                              Oryzias Latipes
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                                                                                                                    Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                    ВJ001358.1 GI:17361625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Plate: LLAM11539 row: i column: 11
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                                                                                                                                                                                                                                                                                                                                                                      Japanese medaka.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitregen). Research Genetics tracking code 027. Note:
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/clone_lib="NIH_MGC_118"
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165 GTCCGCCTGCTGAGG 179
                                                                                       Local Similarity
                                   1 GTCCGCCTGCTGAGG 15
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                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 678.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 683)
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                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.llnl.gov
Plate: LLAM10464 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                             127
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                                                                     Conservative
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                                                                                                                                                   /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 203 c 209 g 144 t
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/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryzias latipes"
/strain="Hd-rR"
                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4538187"
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                                                                                                                                                                                                                                                                                                   /clone_lib="NIH_MGC_91"
                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                    Score 15; DB 10; Length 683; Pred. No. 2.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS; genome survey sequence. Tetraodon nigroviridis.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 848)
                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                         603060993F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210231 5',
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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116D24 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
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NIH-MGC http://mgc.nci.nih.gov/

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BI915042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 845.
Location/Qualifiers
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: LLAM11527
                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                         High quality sequence stop: 840.
                                                                                                                  http://image.llnl.gov
Plate: LLAM11609 row:
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1 (bases 1 to 853)
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                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                  through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. this is a NIH MGC Library."

a 265 c 230 g 195 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                               Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_MGC_122"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Full-length cDNA libraries and normalization Unpublished (2001)
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Li,W.B., Gruber,C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Site_2: ECORV (destroyed): RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (ECORV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIFLMGC Library."
.61 a 269 c 229 g 194 t
                                                                                                      Conservative
                                                                                                                                                                                                                  /tissue_type="placenta"
/tissue_type="placenta"
/note="vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
/note="vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
/note="vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filangelifetech.com URL:
http://fulllength.invitrogen.com"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="LTI_NFL006_PL2"
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Pred. No. 2.8e+03;
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                                                                                                                                                                                                                                                              AA015272 179 bp mRNA linear EST 21-JAN-19 mh30g12.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNP clone IMAGE:444070 5' similar to gb:X16706 FOS-RELATED ANTIGEN 2
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dui
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                           Mus musculus
                                                                                                                                                                                             AA015272.1 GI:1476304
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                                                                                                                                                                                                                                       (HUMAN);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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/clone_lib="G"
/note="Genoscope sequence ID : C0BG075AF01LP1~end : T7"
/note="Genoscope sequence ID : C0BG075AF01LP1~end : T7"
/note="Genoscope sequence ID : C0BG075AF01LP1~end : T7"
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/clone="075K01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:7992574
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                           Bowles, M., Dietrich, N., Dubuque, T.
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S. Dubcovsky, J. Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J. M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Oghhara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE419553 240 bp mRNA linear EST 24-JUL-2000 WWS014.ElR000101 ITEC WWS Wheat Scutellum Library Triticum aestivum
                                                                                                                                                                                                              1 (bases 1 to 240)
Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                   bread wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                         Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="placenta"
/dev_stage="adult"
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/strain="C57BL/6J"
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44 g 47 t
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                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.bs/Scripts/gethtml2.pl?tl=&t2=CM1-FT0051-200 600-281-hl1&t3=2000-06-20&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H. Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CM1-FT0051-200600-281-h11 FT0051 Homo sapiens cDNA, mRNA sequence. BE770021
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Tel: 44 1603 250 2600
Fax: 44 1603 250 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Schuch W
                                                                                                                                                       Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
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International Triticeae EST Cooperative (ITEC)
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                                                                                                          quality sequence start: 19 quality sequence stop: 279.
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                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="FT0051"
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/tissue_type="scutellum callus"
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/cultivar="Novosibirskaya 67"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 395)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse
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                         T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p77T3 vector.
                                                                                                                                                           /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                                                                                                          /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:1067798"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_mammary_gland_NbMMG"
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Search completed: November Job time: 544.591 secs
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1 (bases 1 to 404)

Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Hausner, J., Lai, H., Martin, W., Lai, H., Martin, W., Aramayo, R., Kupfer, D., Gray, J., Lai, H., Martin, W., Lai, H., Martin, W., Lai, H., Martin, W., Lai, H., Martin, M., Lai, H., M., Martin, M., Lai, H., M., Martin, M
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404 bp mRNA linear EST 19-OCT-19917901al.rl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone
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Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
Other_ESTs: i7g0la1.fl
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Query Ma Best Loo Matches	UII 33 te PL	Query M Best Lo Matches	RESULT 1 S-09-437-457-8 Sequence 8, Application US/09 Patent No. 6273893 GENERRAL INFORMATION: APPLICANT: GIORDANO, Anthony APPLICANT: GIORDANO, ANTHONY APPLICANT: MAVIET, ASSISS TITLE OF INVENTION: UNCLEIC TITLE OF INVENTION: INTERACT TITLE OF INVENTION: INTERACT TITLE REFERENCE: 50093/014001 CUGRENT APPLICATION UNMBER: CURRENT FILING DATE: 1999-11 NUMBER OF SEQ ID NOS: 20 SOFTWARE: FRSTSEQ for Window SEQ ID NO		338 444 442 443 443 443 443	3 3 3 3 7 5 5 4	30 31 32 33
atcl	91-8/c 91-8/c 91-8/c 91-8/c 91-8/c 91-8/c APPLICANT: COEN, DONALD M TITLE OF INVENTION: INHIB ICANION MUMBER OF SEQUENCES: 9 CURRENT APPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 21-FEB-199 JD NO:8: LENGTH: 1730 91-8	O 9	quence 8, Application to Carassian Seric Inc. (273893) NEERI INC. (273893) NEERI INC. (273893) PPLICANT: Giordano, IppLICANT: Giordano, IppLICANT: Xavier, ITLE OF INVENTION: ITLE OF INVENTION URRENT APPLICATION URRENT FILING DATE: UMBER OF SEQ ID NO. OFTMARE: FASTSEQ fc Q ID NO. B ID NO. B ID NO. COFTMARE: PASTSEQ fc Q ID NO. COFTMARE: PASTSEQ fc		14.2 14.2 14.2 14.2 14.2		
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US-08-778-494B-91/c
                                                                                                                                                                                               Sequence 92, Application US/08778494B Patent No. 5962272
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                             GENERAL INFORMATION:
                                                          APPLICANT: Diachenko,
APPLICANT: Siebert, I
TITLE OF INVENTION: 1
TITLE OF INVENTION: (
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                                                                                              APPLICANT: Chenchik, Alex
APPLICANT: Zhu, York
APPLICANT: Diachenko, Luda
APPLICANT: Siebert, Paul
                      CORRESPONDENCE ADDRESS:
                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (synthetic)
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
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mes 17; Conserv
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REGISTRATION NUMBER: 38,261
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FILING DATE: 03-JAN-1997
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85.0%; Pred. No. 1.8e+02;
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-778-494B-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 104, Application US/08778494B
; Patent No. 5962272
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; GENERAL INFORMATION:
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                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
              FILING DATE: 03-JAN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/778,494B
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Diachenko
APPLICANT: Siebert,
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chenchik, Alex APPLICANT: Zhu, York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
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APPLICATION NUMBER: US 08/582,562
FILING DATE: 03-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 CCCCGCCGTGCGGCCGCTCG 21
FILING DATE: 03-JAN-1996
                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                              CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2421 N.W. CITY: Gainesville STATE: Florida
                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pace, Doran R. REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 03-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                             32606
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                                                                                                                                                                                                                                              Florida
                                                                                                                                                                                                                                                                           E: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu, York
                                                                                                                                                                                                                                                                                                                                                                                                    Diachenko, Luda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (352) 375-8100
                                                                 03-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                              METHODS AND COMPOSITIONS FOR FULL-LENGTH CDNA
                                                                                                                                                                                                                                                                                                                                               CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.0%;
              US 08/582,562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.2; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 40;
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US-08-778-494B-97
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97,
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                                                                                                                                                            REFERENCE/DOCKET NUMBER: CL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 97:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-8800
INFORMATION FOR SEQ ID NO: 104:
                                                      MOLECULE TYPE:
                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 41 bases
                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION WIBBER: US 08/582,562
FILING DATE: 03-CAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Siebert, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR FULL-LENGTH CDNA TITLE OF INVENTION: CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 CCCCGCCGTGCGGCCGCTCG 21
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                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                       NAME: Pace, Doran R. REGISTRATION NUMBER: 38,261
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/778,494B
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                                                                                                                           LENGTH:
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Diachenko, Luda
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                                                      DNA (synthetic)
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85.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 3;
76.0%; Score 15.2;
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DB 2; Length 41;
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В
; Sequence 2, Application US/09165240A
                  US-09-165-240-2/c
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US-09-568-059-1/c
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LENGTH: 830
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                                                                                                                                                                         Matches
                                                                                                                                                                                             Best
                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.0%; Score 15.2; DB 3; Best Local Similarity 85.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09165240A Patent No. 6087164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY FILE REFERENCE: 9457-0014-999
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/568,059
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/165,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/165,240A CURRENT FILING DATE: 1998-10-01 EARLIER APPLICATION NUMBER: US 08/943,608 EARLIER FILING DATE: 1997-10-03 NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY FILE REFERENCE: 9457-0014-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hochberg, Abraham APPLICANT: Ayesh, Suhail
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 830
TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                     ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                           62 CCCCGCTGTGGGTCCGTCGG 43
                                                                                                                                                                                           Local Similarity
                                                                                                              1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CCCCGCTGTGGGTCCGTCGG 43
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                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 3.0
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                         76.0%;
85.0%;
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                                                                                                                                                                       0;
                                                                                                                                                                                       Score 15.2; DB 4; Length 830; Pred. No. 1.4e+02;
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                                                                                                                                                                       Mismatches
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                                                                                                                                                                     Gaps
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Db
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                                                                                                                                                                                                                                                       US-08-658-665-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-568-059-2
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                                                                                                                                                                                                         Sequence 72, Application US/08658665 Patent No. 5997878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
SEQ ID NO 2
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APPLICANT: Hochberg, Abraham
APPLICANT: Ayesh, Suhail
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Patent No. 6306833
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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Best Local Similarity 85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/568,059
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/165,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY FILE REFERENCE: 9457-0014-999 CURRENT APPLICATION NUMBER: US/09/165,240A CURRENT FILING DATE: 1998-10-01 EARLIER FILING DATE: 1998-10-03 EARLIER FILING DATE: 1997-10-03 NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY FILE REFERENCE: 9457-0014-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hochberg, Abri
APPLICANT: Ayesh, Suhail
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapien
                                         TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 833
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                        CORRESPONDENCE ADDRESS
                                                                                                  APPLICANT: Cox, William I.
APPLICANT: Kauffman, Elizabeth K.
                                                                                                                                              APPLICANT: Pincus, Steven E.
                                                                                                                                                                  APPLICANT: Paoletti, Enzo
                                                                                                                                                                                                                                                                                                                                  50 CCCCGCTGTGGGTCCGTCGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                        Y Match 76.0%;
Local Similarity 85.0%;
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Curtis, Morris & Safford, P.C
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                                         Compositions and Uses 190
                                                                            Recombinant Poxvirus - Cytomegalovirus,
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RESULT 12
US-08-796-101-36
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INFORMATION FOR SEQ ID NO: 72:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J
REGISTRATION NUMBER: 32,1
                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                    MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RESTENOSIS/ATHEROSCLERO TITLE OF INVENTION: PROPHYLAXIS AND THERAPY NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
                                                                                                                                                                                                                                                                                          ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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CITY: N
                                                               APPLICATION NUMBER: FILING DATE: 05-FEE
                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 17; Conserv
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                         NEW YORK
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ZHU, JIANHUI
ERDILE, LORNE
PINCUS, STEVEN
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SPEIR, EDITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPSTEIN, STEPHEN E.
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                                                               05-FEB-1997
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                                                                                  US/08/796,101

 Mismatches

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                                     Matches
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                                                                 Query Match
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                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TOPOLOGY: lir
                                                                                                                                         TOPOLOGY:
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                                   Local Similarity 85. es 17; Conservative
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                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                   NAME: Frommer Esq., William S. REGISTRATION NUMBER: 25,506
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/085,273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
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1 CCCCGCCGTGGGTCCGCCCG 20
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AVENTION: RECOMBINANT POXVIRUS - CYTOMEGALOVIRUS,
AVENTION: COMPOSITIONS AND USES
                                                                                                                                                                                                                                                  : (212) 840-3333
(212) 840-0712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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                              76.0%; Score 15.2; DB 4; Length 837; 85.0%; Pred. No. 1.4e+02; ative 0; Mismatches 3; Indels
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RESULT 15
US-08-441-944A-9
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APPLICANT: SPAETE, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (510) 655-35
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                 APPLICANT: SPAETE, RICHARD TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION TITLE OF INVENTION: OF VIRAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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LENGTH: 961 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                               COMPUTER READABLE FORM:
                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                             656 CCGCGCCGTGCGTCTGCCCG 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                     ZIP:
                                                               COUNTRY:
                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                               Emeryville
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                                                                                                                     4560 Horton Street - R440
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                                                                                                                                                                                                                                                                                                                                                                                                                                           76.0%; Score 15.2; DB 1; Length 961; 85.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHOD OF INCREASING EXPRESSION OF VIRAL PROTEINS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Engless #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,944A

FILING DATE: 16-MAY-1995

CLASSIFICATION NUMBER: US 07/921,807

PRIOR APPLICATION NUMBER: US 07/921,807

FILING DATE: 29-SEP-1992
ATTORNEY/ASENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REFERENCE/DOCKET NUMBER: 3113
REFERENCE/DOCKET NUMBER: 3209.001

TELECOMMUNICATION INFORMATION:
TELECHONE: (310) 655-3542
INFORMATION FOR SED ID MO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 951 base pairs
TYPE: nucleic acid
STRANDENNESS: single
OUE-08-441-944A-9

OUE-Y Match
Best Local Similarity #5.0%; Score 15.2: DB 1; Length 961;
Matches 17: Conservative 0; Mismatches 3; Indels 0; Gaps

QU
1 CCCGCCGTGGGTCCGCCC 20

QU
1 CCCGCCCGTGGGTCCGCCC 20

1 CCCGCCCGTGGGTCCGCCC 675

Search completed: November 2, 2002, 16:50:58

Job time: 22.5455 secs
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
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                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 1.0
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20
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyright (c) 1993 - 2002 Compugen Ltd.
                                                       gb_est1:*
    gb_est2:*
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    gb_gss:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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16.8	16.8	16.8	17.4	17.4	17.4	17.4	17.4	18.4	18.4	18.4	18.4	18.4	18.4	19	20	20	Score		
84.0	84.0	84.0	87.0	87.0	87.0	87.0	87.0	92.0		92.0		92.0	92.0	95.0	100.0	100.0	Query Match	æ	
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A1393367	BB679565	AW447569	AG162212	BF338701	BG687601	BE619884	BG967364	AL553611	BI820274	BI915042	BI767868	BI907636	AV647785	BM463935	BI911023	BE245562	ID		SUMMARIES
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		m	i.	BF338701 602034396	BG687601 602639211	BE619884 601473140	BG967364 602833684	AL553611 AL553611	BI820274 603036831	BI915042 603177231		BI907636 603065545	AV647785 AV647785	BM463935 AGENCOURT	BI911023 603068746	BE245562 TCBAP1E21	Description		

ALIGNMENTS

## RESULT 1 BE245562 FEATURES COMMENT REFERENCE SOURCE ACCESSION DEFINITION LOCUS KEYWORDS VERSION TITLE ORGANISM AUTHORS source Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4556 Fax: 832-825-4038 BE245562 406 bp mRNA linear EST 03-OCT-2001 TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA Unpublished (2000) Contact: Dr. Judith F. Margolin Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project Homo sapiens EST Citation: Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNs. cloping. Methods Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Seq primer: M13 primer Email: clones@txccc.org ##245562.1 GI:9097308 sequence. (bases 1 to 406) /tissue\_type="leukopheresis" /cell\_type="pre-B cell" /dev\_stage="pediatric 2 years" /lab\_host="DHIOB" /organism="Homo sapiens" /db\_xref="taxon.9606" /clone="TcBxp2112" /clone\_lib="Pediatric pre-B cell acute lymphoblastic /sex="male" leukemia Baylor-HGSC project=TCBA" Location/Qualifiers

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BASE COUNT
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Best Local Similarity
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1 (bases 1 to 646)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLAM11547 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      114 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 643 
Location/Qualifiers
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73 a 140 c 130 g 61 t 2 others
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                                                                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range full-length clones and was constructed by C. Gruber full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
209 c 189 g 134 t
                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5217922"
                                                                                                                                                                                                                                                                                         /tissue_type="leukocyte"
/lab_host="DH10B"
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Pred. No. 2.8e+02;
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RESULT 2 BI911023

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ORIGIN

FEATURES

COMMENT

REFERENCE

AUTHORS

SOURCE

KEYWORDS

VERSION

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                                                                                                                     AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                            Homo sapiens
                                                                                                   AV647785.1 GI:9868799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12235 row: e column: 04
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_6445415 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5.39947
5', mRNA securence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
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                                                                                                             http://image.llnl.gov
Plate: LLAM11539 row: i column:
High quality sequence stop: 655.
                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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          /clone="IMAGE:5214802"
                            /db_xref="taxon:9606"
                                                                                        Location/Qualifiers
                                             /organism="Homo sapiens"
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/dev_stage="Adult"
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/clone="GLCBCA03"
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Plate: LLAM11527 row
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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this is a NIH_MGC Library. #
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                                                                                                                                                                                                                                                                                                          full-length clones and was constructed by C. Gruber
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/clone_lib="NIH_MGC_122"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;

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RESULT 8
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Homo sapiens
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BI820274
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Plate: LLAM11609 row: m column: 07
High quality sequence stop: 840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (Invitrogen).
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/clone_lib="NIH_MGC_121"
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                                                                                                         Homo sapiens cDNA clone IMAGE:5178031 5',
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                                                                                                                                                                                                                     Genoscope
                                                                                                                                                                                                                                            Contact: Genoscope
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                                                                                                                                                             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                              BP 191
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AL553611
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Plate: LLAM11443 row: m column: 08
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 885)
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Clone distribution: MGC clone distribution information can be
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/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                             /clone="CS0DI078YB15"
                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruber (Invitrogen). Research Genetic: 021. Note: this is a NIH_MGC Library." a 263 c 245 g 205 t
                                                                                                                                         Location/Qualifiers
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/clone_lib="NIH_MGC_115"
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Pred. No. 1.2e+03
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BASE COUNT
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                                             1 CCCCGCCGTGGGTCCGCCC 19
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                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG967364 768 bp mkwa ilnear ESI 12-JUW-2004 602833684F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4988205 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11000 row: g column: 22
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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                                                                                                                                                                                                          /clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/note="Dyagan: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 252 c 205 g 132 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://fulllength.invitrogen.com"
291 c 262 g 210 t
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                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:4988205"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                              87.0%;
94.7%;
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95.0%;
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 Mismatches

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                                                                                                                                       Score 17.4;
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2.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 917)
                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  602639211F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4762346 5',
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                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                       Homo sapiens
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High quality sequence stop: 763.
Location/Qualifiers
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                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                              human.
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http://image.llnl.gov
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cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Clone_lib="NHI_MGC_68"
/tlssue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life rechnologies."
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/db_xref="taxon:9606"
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94.7%;
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Pred. No. 2.8e+03;
^. wismatches 1;
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM9496 row: p column: 23 High quality sequence stop: 685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF338701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (Clone distribution information can be
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/clone_lib="Null_MGC_59"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (Ti phage-resistant)"
/note="Organ: lung, Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung, Vector: pDNR-LIB
/clone="IMAGE:4182406"
/clone_lib="NCI_GGAP_Brn64"
/tlssue_type="glibblastoma with EGFR amplification"
/lab_host="DH103 (T1 phage-resistant)"
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                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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AG162212
AG162212.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Kohhama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS; GSS (genome survey sequence).

Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-028J06.TJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tc' ki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes DNA, clone: RP43-028J06.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY
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R.Site 2 : FART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (sites)
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                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Prime: Oligo dT Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." a 304 c 331 g 137 t
                                                                                                                                                                                    /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
1 372 c 493 g 14 t 11 others
                                                                                                                                                                                                                                                                         /clone="RP43-028J06.TJ"
                                                                                                                                                                                                                                                                                                /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                       /sex="male"
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                                                                                                   87.0%;
94.7%;
                                                                                                   Score 17.4; DB 12; Length 1110; Pred. No. 2.8e+03;
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RESULT 15

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DEFINITION
ACCESSION
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ORGANISM
Search completed: November 2, 2002, 17:57:14 Job time : 723.455 secs
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                    224 CCCCGCCGTGGGGCTGCCCG 205
                                                                                                                                                                                          Local
                                                                                                                            1 CCCCGCCGTGGGTCCGCCCG 20
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89386 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW447569
AW47569.1 GI:6989356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 11 (4), 626-630 (2001)
21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine {\tt cDNA} libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 245)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,S.C., Bennett Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     row: B column: 11
                                                                                                                                                                                        84.0%; Score 16.8; DB 9; Length 245; 90.0%; Pred. No. 4.7e+03;
                                                                                                                                                                      0;
                                                                                                                                                                      Mismatches
                                                                                                                                                                    Indels
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N_Geneseq_032802:*
1: /SIDSI/gcgdata/ge
2: /SIDSI/gcgdata/g
3: /SIDSI/gcgdata/g
4: /SIDSI/gcgdata/g
4: /SIDSI/gcgdata/g
5: /SIDSI/gcgdata
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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congestive heart failure; ischemic heart	Human; adrenergic receptor; beta2 adrene	receptor betazak					•	d				CHARMONAGA	AT TOWERE			AAH03180	A HOROS 1	AAI.07859	AAL05393	AAL25605	ABA19596	ABA13458	AAK79152	AAL33201	AAF21437	AAA34834	AAF20956	AAA34833	AAF20955	AAK67384	AAK94470	AAH98927	ARI.13276	ABT 13377	AA074060	9000004 01#00100	ABL03417	AALS8986	AAF30281	AAS18444	AAA38339	AAZ00773	AAZ00779	AAZ00776

Result		% Query				
No.	Score	Match	Match Length DB	DB	ID	Description
_	20	100.0	20	21	AAA46128	Human beta2 adrene
2	20	100.0	60	21	AAA38785	beta2
w	20	100.0	2300	20	AAX61116	beta2
4	20	100.0	2305	21	AAA38340	_
رب ر	20	100.0	3451	20	AAZ00774	_
6	20	100.0	3451	20	AAZ00775	Human beta 2-adren
7	20	100.0	3451	20	AAZ00777	_
8	20	100.0	3451	20	AAZ00778	Human beta 2-adren
9	20	100.0	3451	20	AAZ00780	

WPI; 2000-400107/34.

18.4 18.4 118.4 118.4 118.4 118.4 92.0 92.0 92.0 92.0 92.0 20 51 230 1999 2340 3451 3451 AAV52614 AAA38788 AAH79739 AAH27139 AAT93250 AAA38784 Human Interleukin-11 pol Human adenosine re Drosophila melanog Drosophila melanog S. enterica serova The rat beta-actin Reference sequence Perilla flavone sy Human polynucleoti Human beta-adrener Human Human cDNA clone Human Human Human Human Human Human Human Human Human immune/haema Interleukin-11 pol Human Human Human Human Human Human Drosophila melanog Drosophila melanog Human Beta-2 Human nervous syst nervous syst breast cance radenosine re ractor-relat SNP oligonuc immune/haema breast cance beta beta-2-adren beta-2 adren 2 adrenalin r beta2 adrene DNA containi reproductive EST-derived beta beta beta2 adrene full-length 2-adren 2-adren 2-adren pol

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obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; allele-specific oligonucleotide primer; ss. Liggett SB; 25-NOV-1998; 24-NOV-1999; 02-JUN-2000. WO200031307-A1. Homo sapiens. (UYCI-) UNIV CINCINNATI. 98US-0109886 99WO-US27963. ion; asthma; hypertension; ergic receptor; beta2AR; T allele-specific primer #2.

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AAA38785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure.
Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to
                                                                                                                                      (UYCI-) UNIV CINCINNATI
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                                                                                                                                                                                                                                                                                                                                                                                                                 anaphylaxis; chronic obstructive pulmonary disease; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypertension
                                                   WPI; 2000-400107/34.
P-PSDB; AAY99531.
                                                                                                    Liggett SB;
                                                                                                                                                                                                          24-NOV-1999;
                                                                                                                                                                                                                                          02-JUN-2000.
                                                                                                                                                                        25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCCGCCGTGGGTCCGCCTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is an allele-specific oligonucleotide primer lele of the human beta2 adrenergic receptor (beta2AR) gene,
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This sequence represents the human beta2-adrenergic receptor gene, and is amplified by the primers of the invention. The primers are non-self hybridising; contain at least 15 nucleotides (nt) and has a melting temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising; anneals to two distinct segments (separated by at least 400 nt); and generates a homogeneous population of gene segments in a polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 60 BP; 6 A; 24 C; 21 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' beta2AR genes to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a fragment of the T allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 2; 56pp; English.
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asthma; peripheral vascular disorder; neuropsychic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlphalB-adrenergic receptor;
beta2 adrenergic receptor; ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta2-adrenergic receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX61116 standard; DNA; 2300 BP
                                                                                                                                                Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                      Pairs of oligonucleotides for amplifying adrenergic receptor genes
                                                                                                                                                                                                                                                                    Buescher R,
                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                    10-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endocrine-metabolic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            congestive heart failure, ischemic heart disease, arrhythmia, obesity
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                                                                                                                                                                                                                                                                    Insel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r; human; cardiovascular disease;
genetic variation identification; hypertrophy;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence complementary to a template sequence in a DNA polymerase reaction. The primers are used to amplify segments of the alphalB and beta2 adrenzygic receptor genes, particularly to identify genetic variations for diagnosis of disease. Specifically variations in the
              The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (ATI) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern of polymorphisms from the individual with a reference polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA38340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis; drug screening; treatment outcome; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA38340 standard; DNA; 2305 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of genetic alterations not previously amenable to routine, automated and
                                                                                                                                                                                                        Disclosure; Page 124-125; 126pp; English.
                                                                                                                                                                                                                                                                                                                                 WPI; 2000-318010/27.
                                                                                                                                                                                                                                                                                                                                                                        Norberg LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200022166-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-adrenergic receptor-2 gene; coding region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta-adrenergic receptor-2 coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  large-scale sequencing analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reaction (PCR). At least one primer in the pair can extend a 3'-end
                                                                                                                                                                                                                                                encoding specific proteins, with reference polymorphic pattern
                                                                                                                                                                                                                                                                    polymorphic pattern comprising polymorphic positions within genes
                                                                                                                                                                                                                                                                                         Assessing cardiovascular status in humans involves comparing test
                                                                                                                                                                                                                                                                                                                                                                                                                (EURO-) EURONA MEDICAL AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCCGCCGTGGGTCCGCCTG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
  obtained from a population of individuals exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Andersson MK, Lindstrom PHR, Jonsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0104286
98US-0104302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-IB01678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 5
AAZ00774
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CC primers and probes for detecting a polymorphic site may be used as comprising an oblymorphic site may be used as comprisers and probes for detecting genetic polymorphisms or in molecular clibrary arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular cardiovascular in individual's polymorphic pattern reduces or climinates trial and error in selecting a treatment for a particular cardiovascular patient. It also provides the ability to celiminate patients from clinical trials who are predicted to be con-responsive, or at a risk for an adverse resounce, to a particular creatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of that the adverse results can be exclusion of such sub-populations from the treatment group. Beneficial cardiag can be approved for use in the appropriate population, thereby concerns the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. The present conditions from the treatment group is the number of patients required for a clinical trial, which in the conditions of the cost of such trials. The present conditions from the treatment group is the identified to the conditions of the cost of such trials. The present conditions are presents the human beta-adrenery creceptor-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myccardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2305 BP; 495 A; 616 C; 649 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding region (GenBank Y00106/g293708). The polymorphic sites identified are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
                                                                                                                                                                                                                                                                                                                                                                                                  eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta 2-adrenergic receptor DNA variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ00774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA200774 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2068 no insert/G/C and 2070 no insert/C.
                                                                                               mutation
                                                                                                                                                                                                                          кеу
                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729 CCCCGCCGTGGGTCCGCCTG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loca L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                       /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773"
                                               /note= "This nucleotide differs from the wild type
                                                                                               replace(245,a)
                                                                                                                                                                                                  replace(159,t)
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; 100.0%; Pred. No.
                       nucleic acid sequence represented in AAZ00773*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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mutation

replace(565,g)

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mutation
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                                                                                                                                                                            mutation
                                                                                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN
                           30-DEC-1997;
                                                     30-DEC-1998;
                                                                               29-JUL-1999
                                                                                                           W09937761-A1
                                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
                           97DE-1058401.
                                                       98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(1666,c)
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(934,g)
/*tag= d
                                                                                                                                                                replace(2826,g)
/*tag= o
                                                                                                                                                                                                                                                                                                                                                                          replace(2078,c)
/*tag== 1
                                                                                                                                                                                                                                                                                                                                                                                                                               replace(1839,g)
/*tag= k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1568,t)
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AA200773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(1120,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
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                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                   replace(2640,g)
                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                          replace(2110,c)
                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(1221,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "This nucleotide differs from the wild type municia acid sequence represented in AAZ00773"
                                                                                                                                                     "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                   "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *This nucleotide differs
                                                                                                                                                                                                          "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                              "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence represented in AAZ00773'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic
                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                 and results in a change in the corresponding wild type amino acid sequence from an Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wild type amino acid sequence from an Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence represented in {\tt AAZ00773} and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wild type amino acid sequence from an Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residue to Arg residue"
                                                                                                                                      nucleic acid sequence represented
                                                                                                                                                                                                                                                                                                      residue to Thr residue"
                                                                                                                                                                                                                                                                                                                                                nucleic acid sequence represented in AAZ00773
                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           residue to Gln residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequence represented in AAZ00773"
                                                                                                                                                                                             sequence
                                                                                                                                                                                            represented
                                                                                                                                                                                            in AAZ00773
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B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-advencey; receptor sequence variants can be us to develop therapeutics and/or lifestyle drugs. Individual specific be 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1523 CCCCGCGTGGGTCCGCCTG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AACOO773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attention deficit disorder with hyperactivity, eating disorders, e.g. anorexis nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-479048/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoehe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ00775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                method to determine a predisposition for high blood pressure as well as
                                                                                                                                                                                                                                                                                                     neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                                                                                                                                                                                                                                                                                                       neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta 2-adrenergic receptor DNA variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ00775 standard; DNA; 3451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for abnormal blood pressure and other cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene sequences which have hypotensive, cardiant, neuroprotective and in a immunosuppressive activity. The products of the invention are used in a
                                                                                                                                mutation
                                                                                                                                                  Key
                                                                                                                                                                                                                                               SS
                                                                                                                                                                                                                                                                 post-traumatic stress disorder; autonomous nervous system disease;
metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                               Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                            HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCCCGCCGTGGGTCCGCCTG
                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          describes novel variant human beta 2-adrenergic receptor
                                                                                                                              replace(1541,c)
                                                                                            /note- "This nucleotide differs from the wild type
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Timmermann
                                    nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Cys
                  wild type amino acid sequence from residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           otner;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases, including
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AC AAZI
AC AAZI
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D7 O7-0
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BE Humm
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KW Bett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke other conditions that can be
                                                                                                                                                                                  Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g.
                                                                                                                                            neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                                                                                                                                                                                                                                                                                     07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1523 CCCCGCCGTGGGTCCGCCTG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 2a; 27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining an individuals haplotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-479048/40.
                                       Homo sapiens
                                                                                                     metabolic illness; gene therapy; pharmaceutical intervention therapy.
                                                                                                                           post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                       Human beta 2-adrenergic receptor DNA variant 4.
                                                                                                                                                                                                                                                                                                                                                               AAZ00777;
                                                                                                                                                                                                                                                                                                                                                                                                     AAZ00777 standard; DNA; 3451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                 (first entry)
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Pred. No.
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Synthetic

RESULT 8 AAZ00778

ΠŢ

AAZ00778 standard; DNA; 3451 BP

AAZ00778

В

1523 CCCCGCCGTGGGTCCGCCTG

1542

1 CCCCGCCGTGGGTCCGCCTG 20

Matches

Conservative

Mismatches

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to develop therapeutics and/or lifestyle drugs. Individual specific bets 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                  disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be
                                                                                                                                        Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determined include neuropsychiatric disease, such as depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta2-adrenergic receptor gene variants, useful for determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                    determined. The beta 2-adrenergic receptor sequence variants can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myocardial infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-479048/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                        Local
. Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koepke K,
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nucleic acid sequence represented in AAZ00773
and results in a change in the corresponding
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                                 100.0%;
                                                                      100.0%;
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Pred. No.
                                    6.5;
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Gaps
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D,

1523 CCCCGCCGTGGGTCCGCCTG 1542

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                                                                                                                                                       individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                              predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta to develop the agents of the developed. Treatments can be optimized for agents.
                                                                                                                                                                                                                                                                                                 disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                                                                                                                                                                                                                                                        and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Fig 2a; 27pp; German.
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                                                                                                                    Sequence 3451 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta 2-adrenergic receptor DNA variant 5.
                                                          Local
                                                                                                                                                                                                                                                                                                                                                             the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
  1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta2-adrenergic receptor gene variants, useful for
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iliness; gene therapy; pharmaceutical intervention therapy;
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97DE-1058401
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/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                    790 A; 872 C; 895 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Timmermann
                                                          100.0%; Score 20; DB 100.0%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residue to Arg residue"
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                                       0;
                                         Mismatches
                                                                               DB 20;
                                       0;
                                                                             Length 3451;
                                       0;
                                     Gaps
                                         0,
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This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                    anorexia nervosa and bulimia, or post-traumatic stress disorder. Disea of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic
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                                                                                                                                                                                  myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, attention deficit disorder with hyperactivity, eating disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ00780 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-479048/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolic illness; gene therapy; pharmaceutical intervention therapy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta 2-adrenergic receptor DNA variant 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koepke K,
    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
metabolic illnesses, e.g. morbid obesity including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97DE-1058401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wild type amino acid sequence from an residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid sequence represented in AAZ00773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to Arg residue"
                                                                                                                                                                                                                                                                                                            including
                                                                                                                                                      Diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                  which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour,
                                                                                                                                                                                                                                                                                                                                    Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                  Claim 8; Page 11; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liggett SB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allele-specific oligonucleotide primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anaphylaxis; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta2 adrenergic receptor beta2AR C allele-specific primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA38788;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3451 BP; 789 A; 872 C; 896 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used
The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and determine the best treatment.
                                   migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD)
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCI-) UNIV CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity; diabetes; vascular disease; premature labour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to develop therapeutics and/or lifestyle drugs. Individual specific be receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                                                           the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
                                                                                                                                                                                                                                              present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adrenergic receptor; beta2 adrenergic receptor; beta2AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0109886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US27963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                              an allele-specific oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta
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  AAH79739
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                              and activity of proteins related to angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHO) Class I histocompatibility antigen and/or phosphoglycerate kinase. Disorders that may be prevented, alagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4-hydroxybutyrate; dehydrogenase; protein therapy; adenosine triphosphate-dependent RNA helicase; major histocompatibility antigen: MHC; phosphodycerate kinase; immunosuppressive; immunostimulatory; antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
of the bladder, brain,
                                                                                                                                                                                       proteins have potential immunosuppressive, immunostimulatory, antirheumatic, antischerotic, antidiabetic, antiinflammatory, cytostat. antirheumatic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A;
                                                                                                                                                                                                                                                                  nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
                                                                                                                                                                                                                                                                                                           angiopoletin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-418297/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 162; 484pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-2000; 2000WO-US35346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; single nucleotide polymorphism; SNP; angiopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA containing single nucleotide polymorphism SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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                                                                                                                                                                                                                                                                                        histocompatibility antigen and/or phosphoglycerate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for diagnosing and treating, e.g. cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0472688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.0%;
breast, colon and kidney, leukemia), diseases of infection of pathogenic organisms. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                   cytostatic
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25 × 30

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RESULT 12
AAH27139
          Best Local Similarity
Matches 19; Conserv.
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                                                                                                                                                         of mRNA from the nucleus to the cytoplasm, mRNA stabilisation, translational efficiency, and the sequestration of some mRNAs. Therefore modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBPs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP interaction or mRNA functionality; or RBPs that interact with the compounds identified using the gene fragments are potentially useful for therapeutic regulation of gene expression, such as in cases of neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used to alter phenotypic traits such as longevity, appearance, strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Giordano A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000; 2000WO-US30888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200134624-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta-2 adrenergic receptor UTR region with RBP binding ability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH27139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH27139 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;
                                                                             Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  Sequences AAH27132 - AAH27151 represent human gene untranslated regions where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity. RBPs mediate the processing of pre-mRNA, the transport
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 28; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-335904/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids that bind RNA-binding proteins or regulate mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MESS-) MESSAGE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1999;
                                                                                                                            inflammation; metabolic disorders (obesity and diabetes) and bacterial viral infection. The present sequence is one of gene fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         function, useful for therapeutic gene regulation, such as in cases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CCCCGCCGTGGGTCCGCCCG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                               isolated from the human beta-2 adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xavier AK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0437458
                         92.0%;
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 BP
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            0
                           Score 18.4;
Pred. No. 39;
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            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; inflammation;
            1;
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            Indels
                                           Length 230;
            0;
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            Gaps
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            0;
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ID AATS
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AAA38784
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                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthmatic disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-2 adrenalin receptor subtype coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT93250 standard; cDNA to mRNA; 1999 BP
                                              Human beta2 adrenergic receptor beta2AR gene.
                                                                                  05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                            asthmatic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 27-30; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW34320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DAIN ) DAINIPPON PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1996;
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                                                                                                                 AAA38784;
                                                                                                                                                   AAA38784 standard; DNA; 2340 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 ccccccccrcccrcccccc
                                                                                                                                                                                                                                      125 CCCCGCCGTGGGTCCGCCCG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCCGCCGTGGGTCCGCCTG
                                                                                                                                                                                                                                                                     1 cccccccrcccrcccccc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-489627/45
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-0072914.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       92.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawashima H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                       Score 18.4;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nomura A,
                                                                                                                                                                                                                                                                                                                                           DB 18;
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This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used in screening for agonists and antagonists, which are useful in researching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases
Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5q31(12); disease predisposition; asthma; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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AAV52614
ID AAV
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XXX
                                                          RESULT 15
                                                                                                                                         Matches
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                       The present sequence is a fragment of the C allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, and so the standard of the second congestive heart failure, ischemic heart disease, arrhythmia, obesity, and is the second congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; ds.
                                                                                                                                                                                                                      diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                     St quence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congestive heart failure; ischemic heart disease; arrhythmia;
                                                                                            1523 CCCCGCCGTGGGTCCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCI-) UNIV CINCINNATI.
             AAV52614;
                                    AAV52614 standard; cDNA; 3451 BP
                                                                                                                                                                                                            determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                             hypertension
                                                                                                                                                    Local
                                                                                                                  1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                   Similarity
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0109886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "beta2 adrenergic receptor"
/note= "no stop codon given at 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 1487..2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1588,.2340
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1487..1546
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                                                                                                                                                   92.0%;
                                                                                             1542
                                                                                                                                         0
                                                                                                                                                   Score 18.4;
Pred. No. 3
                                                                                                                                          Mismatches
                                                                                                                                                                DB 21;
                                                                                                                                          1;
                                                                                                                                                                Length 2340;
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                                                                                                                                          Indels
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      Search completed: November Job time; 83.7273 secs
                                                                                                Matches
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cc second alleles of the beta 2-adrenergic receptor gene and (b) classifying an individual as susceptible if first and second classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor gene alleles may be dentified by any known method e.g. denaturing gel electrophoresis or pck amplification (see also AAVS2615-17). Identification preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also comprises determining nucleotide sequences of these portions (e.g. to adverse determining nucleotide sequences of these portions (c.g. by automated sequence analysis). The invention identifies a known to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and individuals because of for xard and analysis of the encoded protein can be either Arg or Gly, and individuals because of for xard and analysis.
                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW75777) having an arginine residue at position 16. A novel methor for identifying individuals susceptible to adverse responses to regular administration of beta-agonists comprises: (a) identifying in a genomic nucleic acid sample from the individual first and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patients homozygous for allele encoding Arg at position 16 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boushey H,
Martin RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphism; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta-2-adrenergic receptor cDNA.
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1523 CCCCGCCGTGGGTCCGCCCG 1542
                                                                                                                                                                                                                                                           Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA sequence codes for human beta-2-adrenergic receptor (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 33-35; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta2-adrenergic receptor protein
                                                                                                                                                                                                                                                                                                                         individuals homozygous for Argl6 are more susceptible.
                                                                                                                                                               Local Similarity
                                                             1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chinchilli VM, Drazen JM,
                                                                                                                                    Conservative
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                                                                                                                                                            92.0%;
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                                                                                                                                                               Score 18.4;
Pred. No. 3;
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                      Score
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-165-240-1

US-09-168-059-1

US-09-168-059-1

US-09-168-059-2

US-09-168-059-2

US-08-483-232-2

US-08-483-232-2

US-08-481-24-24

US-08-910-041-24

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US-09-100-715-24

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US-09-018-635-28
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                                                                                                      Sequence 31, Appl
Sequence 3, Appl
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Patent No. 5457037
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    APPLICANT: VIITAMEN, PAUL V.
APPLICANT: JORDAN, DOUGLAS B.
TITLE OF INVENTION: RIBOPLAVIN SYNTHASE GENES AND ENZYMES
FILE REFERENCE: CL-1083-B
CURRENT APPLICATION NUMBER: US/09/277,700
CURRENT APPLICATION NUMBER: US/09/277,700
                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                          Sequence 31, Application US/09277700 Patent No. 6350597
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
EARLIER APPLICATION NUMBER: 08/912,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: MICROSOFT WO:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                 17 CGCCGCCGTGTCTCCGCCTG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                                                                                                                                                                                              1 cccccccreeercccccre 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                                                                                                                                    Local Similarity
es 17; Conserv
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CITY: WILMINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NO.
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                                                                                                                                                                                                                                                                                                                  76.0%; Score 15.2; DB 3; Length 684; 35.0%; Pred. No. 1.4e+02;
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                                                                                                     SEQ ID NO 1
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Query Match
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                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09568059 Patent No. 6306833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
LENGTH: 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: arabidopsis US-09-277-700-31
                                                                                                                                                   CURRENT APPLICATION NUMBER: U5/09/568,059
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/165,240
PRIOR FILING DATE: 1998-10-01
                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY FILE REFERENCE: 9457-0014-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                               APPLICANT: Hochberg, Abraham APPLICANT: Ayesh, Suhail
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                                                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
                                          TYPE: DNA
ORGANISM: Homo Sapien
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Office 97
SEQ ID NO 31
LENGTH: 684
TYPE: DNA
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Patent No. 6087164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/165,240A CURRENT FILING DATE: 1998-10-01 EARLIER RELICATION NUMBER: US 08/943,608 EARLIER FILING DATE: 1997-10-03 NUMBER OF SEQ ID NOS: 11
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                                                                                    LENGTH: 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                         62 CCCCGCTGTGGGTCCGTCGG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCCCCCGTGGGTCCGCCTG 20
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                                                                                                            FastSEQ for Windows Version 3.0
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Best Local Similarity

76.0%; 85.0%;

Score 15.2; DB 4; Pred. No. 1.4e+02;

Length 830;

Matches

17;

Conservative

0;

Mismatches

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Indels

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US-08-483-232-24
; Sequence 24, Application US/08483232
; Patent No. 5656431
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                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-568-059-2
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SEQ ID NO 2
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LENGTH: 833
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APPLICANT: Ayesh, Suhail
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
FILE REFERENCE: 9457-0014-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09568059 Patent No. 6306833
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/165,240 PRIOR FILING DATE: 1998-10-01 NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 9457-0014-999
CURRENT APPLICATION NUMBER: US/09/568,059
CURRENT FILING DATE: 2000-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Patent No. 6087164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/165,240A CURRENT FILING DATE: 1998-10-01 EARLIER APPLICATION NUMBER: US 08/943,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 9457-0014-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hochberg, Abraham APPLICANT: Ayesh, Suhail
                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapien
                                                                                                  50 ccccccrcrcccrcccrccc 31
                                                                                                                    1 CCCCGCCGTGGGTCCGCCTG 20
                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 CCCCGCTGTGGGTCCGTCGG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watch 76.0%; Score 15.2; DB 3; Length 833; Local Similarity 85.0%; Pred. No. 1.4e+02; Pred. 17; Conservative n. Michael 17; Conservative n. Michael 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 cccccccrcccrccccccc 20
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                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                    833
                                                                                                                                                                                            Similarity
                                                                                                                                                                         Conservative
                                                                                                                                                                               76.0%; Score 15.2; DB 4; Length 833; 85.0%; Pred. No. 1.4e+02;
                                                                                                                                                                        0;
                                                                                                                                                                  Mismatches
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                                                                                                                                                                Indels
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US-08-485-938A-24
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                                                                                                                    Sequence 24, Application US/08485938A Patent No. 5847088
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.0:
17; Conservative
                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (312) 474-044
TELEX: 25-3658
INFORMATION FOR SEQ ID NO:
                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                            APPLICANT: APPLICANT:
      TITLE OF INVENTION:
                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
                                                                                                                                                                                                          432 CCCCGCCGTGGGACCTTCTG 451
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-OCT-PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     1 CCCCGCCGTGGGTCCGCCTG 20
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                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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:: Illinois
               Le Trong, Hai
Tjoelker, Larry W.
Wilder, Cheryl L.
                                                        Eberhardt, Christine D. Gray, Patrick W.
                                                                                         Cousens, Lawrence S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (312) 474-0448
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linear
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                                                                                                                                                                                                                                                                                                                                             468..1734
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Le Trong, Hai
Tjoelker, Larry V
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Eberhardt, Christine D.
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                                                                                                                                                                                                                                                                                76.0%;
85.0%;
Platelet-Activating Factor
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                                                                                                                                                                                                                                                                             Score 15.2; DB 1;
Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                         Length 1876;
                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                            Gaps
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TITLE OF INVENTION:

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US-08-910-041-24
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US-08-485-938A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/133
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 584708Band, Greta E
REGISTRATION NUMBER: 35,302
                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         432 CCCCGCCGTGGGACCTTCTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                            ADDRESSBE: Marshall, O'IOGE, COLLEGE STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TODOLOGY: 1:505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                      Chicago
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25-3658
United States of America
                                                                                                                                                                                             Eberhardt, Christine D. Gray, Patrick W.
                                                                                                                                                                                                                            Cousens, Lawrence S.
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                                                      Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; DB 2; Length 1876;
Pred. No. 1.3e+02;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 12
US-09-328-474-24
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Patent No. 6045794
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pair
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,547 REFERENCE/DOCKET NUMBER: 2786 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300 TELEFAX: (312) 474-0448
                                                                                                                                                                   APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet.
TITLE OF INVENTION: Acetylhyc
NUMBER OF SEQUENCES: 30
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APPLICANT:
                                                                                                                                                   CORRESPONDENCE ADDRESS:
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      OPERATING SYSTEM:
                                                                 ZIP:
                                                                              COUNTRY:
                                                                                                           CITY: Chicago
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                         STREET:
                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCCGCCGTGGGTCCGCCTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/318,905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                60606-6402
                                                                                             Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I: 1876 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60606-6402
                                                                                                                     6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                       Application US/09328474
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                                                                         United States of America
                                                                                                                                                                                                                             Gray, Patrick W.
Le Trong, Hai
Tjoelker, Larry W.
                                                                                                                                                                                                                                                                          Eberhardt, Christine D.
                                                                                                                                                                                                                                                                                          Cousens, Lawrence S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
IBM PC COMPATIBLE
SYSTEM: PC-DOS/MS-DOS
                                                                                                             Marshall, O'Toole, Gerstein, Murray & Borun
00 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.0%;
85.0%;
                                                                                                                                                                      Acetylhydrolase
                                                                                                                                                                                          Platelet-Activating Factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.2; DB 2; Length 1876; Pred. No. 1.3e+02;
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US-09-100-546-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRINT APPLICATION DATA: APPLICATION NUMBER: US/09/100,546
                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                 NUMBER OF SEQUENCE ADDRESS:

CORRESPONDENCE ADDRESS:

Anneessee: Marshall, O'Toole,

Tower, 233
                                                                                                                                                                           STREET: Chicago
                                                                                                                                                                                                                                                                      APPLICANT: Gray, Patrick W.

APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.

APPLICANT: Wilder, Cheryl L.

TITLE OF INVENTION: Platelet-Activating Factor
APPLICANT: Acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 24:
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
                                                            SOFTWARE:
                                                                                          MEDIUM TYPE:
COMPUTER: IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 CCCCGCCGTGGGACCTTCTG 451
CLASSIFICATION:
                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/483,232 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                           60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                   6099836
                                                                                                                                                                         Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09100546
                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                             Cousens, Lawrence S.
Eberhardt, Christine D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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06-OCT-1993
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                                                                                                                                                                                                                                                             Acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%; Score 15.2; DB 3; Length 1876; 85.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/318,905
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0; Mismatches 3;
                                                                                                                                                                                                  South
                                                                                                                                                                                                             Gerstein, Murray & Borun
                                                                                                                                                                                               Wacker Drive
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Patent No. 6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cousen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                           FILING DATE: 06-OCT-PRIOR APPLICATION DATA:
                                                                 PRIOR APPLICATION DATA:
                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 24:
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APPLICANT:
APPLICANT:
APPLICANT:
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ADDRESSEE: Marshall, O'Toole,
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                      APPLICATION NUMBER: US 0
FILING DATE: 06-OCT-1994
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FILING DATE:
         APPLICATION NUMBER:
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                                                                                    CLASSIFICATION:
                                                                                                      FILING DATE:
                                                                                                                                                 SOFTWARE:
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                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                CITY: Chicago
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APPLICATION NUMBER:
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                                                                                                                                                                                                                      60606-6402
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6146625
                                                                                                                                                                                                                                                  Illinois
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                                                                                                                                        PatentIn Release #1.0,
                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                         Le Trong, Hai
                                                                                                                                                                                                                                                                                                                                                                                                          Gray, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                      Eberhardt, Christine D.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cousens, Lawrence S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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 06-OCT-1993
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                                                                                                                                                                                                                                                                                                                                   Acetylhydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.0%; Score 15.2; DB 3; 85.0%; Pred. No. 1.3e+02; ... wismatches 3;
       US 08/133,803
                                                    US 08/318,905
                                                                                                              us/09/010,715
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                                                                                                                                                                                                                                                                                 Gerstein, Murray & Borun
                                                                                                                                       Version #1.25
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RESULT 15
US-09-577-758-24
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                                        APPLICATION NUMBER: US 08/133,80:
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6203790and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/3:
TELECOMMUNICATION INFORMATION:
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Patent No. 6203790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
09/010,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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APPLICANT:
TELEX:
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            TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
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CITY: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 CCCCGCCGTGGGACCTTCTG 451
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LENGTH: 1876 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/577,758
                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                   RY: United States of America 60606-6402
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 25-3658
                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eberhardt, Christine D. Gray, Patrick W. Le Trong, Hai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cousens, Lawrence S.
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                                                            Matches
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Matches 17; Conserv
                                                                                    Query Match
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pair
TYPE: nucleic acid
432 CCCCGCGTGGGACCTTCTG 451
                                                                                                                                                           FEATURE:
                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                            NAME/KEY:
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                         1 CCCCGCCGTGGGTCCGCCTG 20
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Search completed: November 2, 2002, 16:50:59 Job time: 19.5455 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                      AL281595 Tetraodon
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## ALIGNMENTS

FEATURES COMMENT VERSION KEYWORDS DEFINITION ACCESSION RESULT 1 AV647785 LOCUS REFERENCE SOURCE JOURNAL MEDLINE TITLE AUTHORS ORGANISM source Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) This clone Eukaryota; Mammalia; E Homo sapiens AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.

AV647785 EST AV647785.1 GI:9868799 (bases 1 to 427) hanzg@chgc.sh.cn lone is available at CHGC in Shanghai. Location/Qualifiers /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI" /tissue\_type="corresponding non cancerous liver tissue" /dev\_stage="Adult" /lab\_host="SOLR" /organism="Homo sapiens" /db\_xref="taxon:9606" /clone\_lib="GLC" /clone="GLCBCA03" ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BASE COUNT

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RESULT 3
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81767868 848 bp mRNA linear EST 25-SEP-2001 603060993F1 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5210231 5',
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov Plate: LLAM11539 row: i column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: ogapbs r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 659)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI907636.1 GI:16170473
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198 c 194 g 140 t
                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                        1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="leukocyte"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5214802"
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               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                              603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                  BI915042
DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institutes of Health, Mammalian Gene Collection (MGC)
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BI767868.1 GI:15759446
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1 (bases 1 to 848)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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265 c 230 g 195 t 1 others
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                     High quality sequence stop: 839
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                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Organ: pooled brain, lung, testis; vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECCRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (ECCRV site is
                                                                                                                                               /clone="IMAGE:5178031"
/clone_lib="NIH_MGC_115"
                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                            /lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 2.1e+02;
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sequence.
BE245562
                                               BE245562 406 bp mRNA linear ETCBAP1E2132 Pediatric pre-B cell acute lymphoblastic
                                                                                                                                                                                                                                                         20;
                        Baylor-HGSC project=TCBA HOMO sapiens cDNA clone TCBAP2132, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                        183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                         a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="LTI_NFL006_PL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CSODIO78YB15"
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                                                                                                                                                                                                                                                                   100.0%;
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Pred. No. 2.1e+02;
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VERSION

GI:9097308

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REFERENCE
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      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 646)
                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                 Homo sapiens
                                                                                                                                                                                                603068746F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217922 5',
                                                                                                                                                BI911023.1 GI:16174544
                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                                                                                                         BI911023
                                                                                                          uman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: clones@txccc.org
Citation: Carrincl.P. and Hayashizaki.Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 832-824-4536
Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Dr. Judit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Double-Stranded CDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsami T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997) 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGGAGGGAGGAGGAGGAG(T)VN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3^\prime;\ V=A,C,G;\ N=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       יבעגפווום Baylor-HGSC project=TCBA"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT(C) 3']
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Pediatric pre-B cell acute lymphoblastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="leukopheresis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="TCBAP2132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                92.0%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No. 8.7e+02;
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TITLE
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les 19; Conserv
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                       AL281595.1 GI:8019918
GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                        Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
                                                                                                                                                                                                                                Weissenbach, J.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                   Tetraodontidae;
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: LLAM11547 row: k column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                      (bases 1 to 839)
                                                                                                                                                                                                                                                                                              (bases 1 to 839)
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209 c 189 \sigma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2-3.3 kb.
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/clone="IMAGE:5217922"
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/lab_host="DH10B"
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Pred. No. 8.7e+02;
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(bases 1 to 839)

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                                                                                                                                                                                                                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
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2 (bases 1
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                               /note="Genoscope sequence ID : COAG177DF04SP1~end PUC-Ori"
                                                                       /clone_lib="G"
                                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
                                                                                          /clone="177L08"
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AGENCOURT_6445415 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539947 TRAKE SECTION ACCURATION OF THE PROPERTY OF
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Similarity 94.7%;
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/clone="t53821"
/clone="t5"
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.4; DB 12; Pred. No. 2.2e+03;
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Pred. No. 2.2e+03;
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VERSION

BM463935.1 GI:18512977

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COMMENT
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BB870361/c
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                                                                                   JOURNAL
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                                                                                                    Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                      Contact: Yoshihide Hayashizaki
                                                                              Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB870361 RIKEN full-length enriched, 14 days embryo lung Mus
musculus cDNA clone G630020K24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM12235 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcwV-SporT6; Site_1: Not1;
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/db_xref="taxon:9606"
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Pred. No. 2.2e+03;
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ORIGIN

COMMENT

Contact: Yoshihide Hayashizaki

KEYWORDS

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RESULT 14
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                                                      Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Washiliki, W. Vonoda, V. Thilbaua, W. Thilb
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URL:http://genome.gsc.riken.go.jp/
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
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/db_xref="taxon:10090"
/clone="G630020K24"
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musculus cDNA clone G630033L09 5', mRNA sequence.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al
                        Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDMAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/strain="C57BL/6J"
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e mouse tissues.
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                                                                                                     Conservative
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                                                                                                                                                                                                                                /tissue_type="lung"
/dev_stage="14 days embryo"
111 c 106 g 61 t
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                   lung"
                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, 14 days embryo
                                                                                                                                                                                                                                                                                                                                                                 /clone="G630033L09"
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                                                                                                                             84.0%;
90.0%;
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                                                                                                     0; Mismatches
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Pred. No. 3
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/cgn2_6/ptodata/2/ina/sA_COMB.seq:*
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4 US-08-943-731-198
1 US-08-978-182-2
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2 US-08-958-88-1
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LENGTH:

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SOFTWARE: FastSEQ for Windows Version 4.0

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## ALIGNMENTS

RESULT 1 US-09-437-457-8/C

Sequence 8, Application US/09437457 Patent No. 6273893

GENERAL INFORMATION:
APPLICANT: Giordano, Anthony
APPLICANT: Xavier, Ashish
TITLE OF INVENTION: HOLLEIC ACID SEQUENCES AND METHODS FOR
TITLE OF INVENTION: INTERACTIONS THAT AFFECT RNA/RNA BINDING PROTEIN
TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
FILE REFERENCE: 50093/014001
CURRENT APPLICATION NUMBER: US/09/437,457
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 20

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US-09-404-650-1
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                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                   SEQ ID NO 1
                                                                               APPLICANT: Dietrich, Paul S.
APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOUTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                         Sequence 1, Application US/09404650 Patent No. 6309858
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Best Local
NAME/KEY: CDS
                FEATURE:
                           ORGANISM: Homo sapiens
                                                                 LENGTH: 6816
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Similarity 100.0%; Pred. No. 2.5;
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; OTHER INFORMATION: CDC 1551 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence US-09-103-840A-2
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SEQ ID NO 2
                 Matches
                                               Query Match
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09103840A Patent No. 6294328
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Matches 17; Conserv
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                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                            APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAM SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEO LD MOS: 12
NUMBER OF SEO LD MOS: 12
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                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
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LOCATION: (192)..(6755)
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TYPE: DNA
     79.0%;
Local Similarity 89.5%;
les 17; Conservation
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Local Similarity 89.5%;
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 198, Application US/08943731 Patent No. 6265157 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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                                                                                                                                                                                                                                                                                                                   APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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CLASSIFICATION:
             APPLICATION NUMBER: US/08/943,731 FILING DATE: 03-OCT-1997
                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                               COUNTRY:
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ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                   EARLY, JAMES
KORKKO, JARMO
                                                                                                                                                                                                                                                                                                                                                                                                                                              PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELTAS, CONSTANTINOS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPOTILA, LORETTA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROCKOP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARSON, ANDREA W.
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89.5%;
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Pred. No. 42;
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RESULT 7
US-08-390-858B-8
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                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
              MOLECULE TYPE:
                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 654 base pairs
TYPE: nucleic acid
FEATURE:
                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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LENGTH: 420 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
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                                    STRANDEDNESS:
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                                                                                                                                                      NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                      FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     TELEFAX:
                                                                                                                                  TELEPHONE:
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VENTION: Bcl-2 Gene Inhibitory Element Binding
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                                                                                                                (619) 535-9001
519) 535-8949
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                                         double
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    Mismatches

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; LIBRARY: TLYMNC
; CLONE: 3003826
US-08-978-182-2
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                                                             Matches
                                                                                        Query Match
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Hillman,
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261 GGCGGTGGGCGCCTCAGCAG 242
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                      Match 76.0%;
Local Similarity 85.0%;
                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                         TYPE: nucleic acid
                            1 GGCTGGGGGGCGCCTCAGCGG 20
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LOCATION:
                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: Herewi CLASSIFICATION: 435
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CITY: Palo Alto
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                                                          Conservative
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                                                                                                                                                                             linear
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                                                                Score 15.2; DB 2; Length 1926; Pred. No. 2.1e+02;
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                                                        Mismatches
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                                                     Indels
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US-09-205-681-2/c

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Db
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                                                                                                                                                                                  Sequence 7, Application US/08104072B Patent No. 5639948
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Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                       APPLICANT: Michiels, Frank
APPLICANT: Morioka, Sinji
APPLICANT: Morioka, Sinji
APPLICANT: Komeri, Trees
APPLICANT: Komari, Tosihiko
TITLE OF INVENTION: Stamen-specific Promoters from Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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APPLICANT: Hillman, Jennifer L.
                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  261 GCCGGTGGGCGCCTCAGCAG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: TLYMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
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APPLICATION NUMBER:
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ADDRESSEE: Incyte Pharmaceuticals, Inc
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                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mathur, Preete TITLE OF INVENTION: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                 1 GGCTGGGGGGCGCCTCAGCGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/205,681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
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Minneapolis
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               3: Merchant & Gould
3100 No. 5639948west Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
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Pred. No. 2.1e+02;
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RESULT 11
US-08-351-413-8
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                                                                                                                                 Matches 17;
                                                                                                                                             Query Match
Best Local Similarity
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                                                              1874 GGCGGGGGGGCGCTCGGCGG 1893
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LENGTH: 2370 base pairs
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REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
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ATTORNEY/AGENT INFORMATION:
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                                                                                           1 GGCTGGGGGGCGCTCAGCGG 20
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                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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OTHER INFORMATION:
OTHER INFORMATION:
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OPERATING SYSTEM:
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EDNESS: double
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                                                                                                                              Conservative
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1748..1755
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                        76.0%; Score 15.2; DB 1; Length 2370; 85.0%; Pred. No. 2.1e+02;
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promoter"
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                                                                                                                            Mismatches
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Sequence 8, Application US/08351413 Patent No. 5750867

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US-08-351-413-8
        Best Local Similarity 85.0 Matches 17; Conservative
                                           Query Match
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APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
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                                                                                                                                                           FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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LENGTH: 2370 base pairs
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FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            FEATURE
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LOCATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
 76.0%; Score 15.2; DB 1; Length 2370; 85.0%; Pred. No. 2.1e+02; ative 0; Mismatches 3; Indels 0
                                                                               /label= ATG
/note= "ATG start of translation of rice T42 gene"
                                                                                                                                                             /note= "transcription initiation
site determined by primer extension"
                                                                                                                                                                                                                                                     /note= "TATA Box"
                                                                                                                                                                                                                                                                                                                                      /label= PT42
/note= "sequence comprising anther specific
promoter PT42"
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                                 FEATURE:
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NAME/KEY:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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FILING DATE: 12-JUN-
PRIOR APPLICATION DATA:
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PRIOR AT TICATION NUMBER: 1
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
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OTHER INFORMATION:
OTHER INFORMATION:
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                                        OTHER INFORMATION: /label= TATA Box"
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LOCATION: 1780
               NAME/KEY:
                                                                              LOCATION: 1748..1755
                                                                                                                                                                                                                           ORGANISM: Oryza sativa
STRAIN: Akihikari
                                                                                             NAME/KEY:
                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)
TELEX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: bir Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                      2370 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 205-8050
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                                                                                                                                                                             1..1808
                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                           NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUN-1992
                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                          /label= PT42
/note= "sequence comprising anther specific
promoter PT42"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/970,849
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US-08-795-868-13/c
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                                                       Matches
                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NERAL INFORMATION: Lee, Mu-En
APPLICANT: Lee, Mu-En
APPLICANT: Hsieh, Chung-ming
APPLICANT: Hsieh, Chung-ming
TITLE OF INVENTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1874 GGCGGGGGGGCGCGTCGGCGG 1893
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                                                                     Local Similarity
                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
               1 GGCTGGGGGCGCCTCAGCGG 20
                                                                                                                                    LOCATION: 3...198
OTHER INFORMATION:
                                                                                                                                                NAME/KEY: Coding Sequence LOCATION: 3...1983
                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06-FEB-1997
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: FastSE
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                                                   Conservative
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                                           76.0%; Score 15.2; DB 2; Length 2793; 85.0%; Pred. No. 2.1e+02; tive 0; Mismatches 3; Indels 0
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85.0%;
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/note= "ATG start of translation of rice T42 gene"
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site determined by primer extension"
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Pred. No. 2.1e+02;
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; NAME/KEY: CDS
; LOCATION: (3)...(1985)
US-09-303-069-13
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                                                                                   Query Match
Best Local Similarity
Matches 17; Conserve
                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/990,140A
CURRENT FILING DATE: 1997-12-12
EARLIER APPLICATION NUMBER: US 60/033,151
EARLIER FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 13
                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (97)
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) and Human TITLE OF INVENTION: eIF4GF-like Protein (p97) Genes FILE REFERENCE: 1488.0700001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Olsen, Henrik S.
APPLICANT: Ruben, Steven M.
APPLICANT: Sonenberg, Nahum
APPLICANT: Methot, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09303069A Patent No. 6350592
                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/303,069A
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: US 09/134,250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, Mu-En
APPLICANT: Hsieh, Chung-Ming
TITLE OF INVENTION: SINGLE GENE ENCODING AORTIC-SPECIFIC AND STRIATED-SPECIFIC
FILE OF INVENTION: MUSCLE CELL ISOFORMS AND USES THEREOF
FILE REFERENCE: 05433/039001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rom, Eran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2793
189 GGCTGGCGGCGGCTCGGCGG 170
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                                       1 GGCTGGGGGCGCCTCAGCGG 20
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                                                                                 Conservative
                                                                                           76.0%; Score 15.2; DB 3; 85.0%; Pred. No. 2.1e+02;
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                                                                             Mismatches
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                                                                                                              DB 3; Length 3032;
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Search completed: November 2, 2002, 17:08:37 Job time : 1076.55 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
                                                                                                                                                                No.
         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             Score
      Match Length DB
    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
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BG284879
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BI911023 603068746
BB386852 BB386852
AV647785 AV647785
BI907636 603065545
      BG284879 602409113
BI915042 603177231
AL553611 AL553611
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BI722560 1031062g0
BI527454 1024081G0
BI719349 1031042H1
BG645027 1024008E0
BG845026 1024008E0
BG845026 1024008E0
BF864370 963051B07
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BF866118 963066F01
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16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	16.8	17	17
	84.0																									85.0	85.0
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AI916036	AI209019	AA037568	H21861	H28433	AA577199	R28179	R55199	BI035865	AI189106	AA992754	AW297631	R25414	AI273229	AI073807	AZ769071	BF340043	AA399291	H45279	AA831285	AA725280	AA724980	BB311008	AV362547	N91498	AA648867	1954	C84644
AI916036 wi44c02.x	2X3#501.	71170911.5	7074007	054005 6		75.000.5	176409 1102	BT035865 TL5-WT022	0004603.	AA992754 0+84600 s	AW297631 [IT-H-BW0-	50007	g 45h02	v (1069/12	1M056951	~ .	2+53001	H45279 vo65h06 v1	2040300	25280 ail6606.	ai08d09	00	7 AV362547	2a91a11	648867 ns37a08 s	1954411 HVSMEmC	C84644 C84644 Osta

## ALIGNMENTS

	FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	BE245562/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Homo sapiens" /db_xref="taxon:9606" /clone="mcBAP2132" /clone_llb="pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA" /sex="malle" /tissue_type="leukopheresis" /cell_type="pre-B cell" /dev_stage="pediatric 2 years" /lab_host="pH10B"	trans Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4536 Fax: 832-825-4038 Email: clones@txccc.org Citation: Carninci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Seq primer: M13 primer. Location/Qualifiers 1. 406	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (Dases 1 to 406)  Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Glibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project Unpublished (2000) Contact: Dr. Judith F. Margolin	BE245562 406 bp mRNA linear EST 03-OCT-2001 TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA sequence. BE245562 BE245562.1 GI:9097308 EST. human. Homo sapiens

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ACCESSION
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Location/Qualifiers
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Plate: LLAM11547 row: k column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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(Invitrogen). Research Genetics tracking code 027. Note:
this is a NHE_MGC Library."
a 209 c 189 g 134 t
                                                                                    non-activated adult donors. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range full-1-as, kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics trackers and constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen). Research Genetics trackers are constructed by C. Gruber (Invitrogen).
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                                                                                                                                                                                                                                                                          /note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5217922"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leukocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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a 140 c 130 g 61 t 2 others
                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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ORIGIN BASE COUNT FEATURES

COMMENT

JOURNAL AUTHORS REFERENCE

KEYWORDS

RESULT 2

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh.M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., IZawa,M., Kawai,J.,
Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., IZawa,M., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                   further details.
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(bases 1 to 240)
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prepared and sequenced in Mouse Genome Encyclopedia
                                   /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                   /tissue_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                   cerebellum"
                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                               one="C230048L24"
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Query Match
Best Local Similarity
Whiches 19; Conserva
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AV647785/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                    Contact: Zeguang Han Chinese Mational Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21625106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV647785 GLC Homo sapiens cDNA clone GLCBCA03 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV647785.1 GI:9868799
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                Conservative
                                                                                                         80 a
                                                                                                                                                                                                                                                                                                                         clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                      hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLC I. 77 c
                                                                                                                            /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                   /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
                                                                                                                                                                                                             /clone="GLCBCA03"
/clone_lib="GLC"
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                 LOCation/Qualifiers
                                                                                                                                                           /lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                               is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primed with a primer [5'
                                 92.0%;
                                                                                                       149 c
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              0; Mismatches
                             Score 18.4; DB 9;
Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;
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                                          DB 9; Length 427;
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         0;
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       Gaps
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       0;
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REFERENCE

AUTHORS

SOURCE KEYWORDS VERSION ACCESSION SGOO В Š

ORIGIN

BASE COUNT

FEATURES

COMMENT

MEDLINE JOURNAL TITLE

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В
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                                                                                                          ACCESSION
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AUTHORS
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                                ORGANISM
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                                                                                                                                                                                                                                                                                               1 GGCTGGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                    EST
                                                                                                                                602409113F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4538187 5',
                            Homo sapiens
                                                                                    BG284879.1 GI:13036277
                                                                                                        BG284879
                                                                                                                        mRNA sequence.
                                                                                                                                                                BG284879
                                                numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov Plate: LLAM11539 row: i column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI907636.1 GI:16170473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI907636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 659)
                                                                                                                                                                                                                                                                                                                                                                                                                                    127 a
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cloning). A 1.2-3.3 kb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone~"IMAGE:5214802"
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Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                          683 bp
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                                                                                                                                                            mRNA
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                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                     Length 659;
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FEATURES
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BI915042/c
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                                                                                                                                                                Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                         High quality sequence stop: 840.
                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                               Plate: LLAM11609 row: m column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI91504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5
                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI915042.1 GI:16179135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db_xref="taxon:9606"
/clone="IMAGE:5241774"
                                            /organism="Homo sapiens"
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/lab_host="DH10B (phage-resistanty"
/note="Organ: prostate; Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                       Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 1.3e+03;
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148 GGCTGGGGGGCGCCTCAGCAG 129

1 GGCTGGGGGGCGCCTCAGCGG 20

Matches

Local Similarity

Conservative

Mismatches

Length 950;

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ORIGIN
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL553611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI078YB15 5
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91006 EVRY cedex - France
                                                                              http://fulllength.invitrogen.com" 291 c 262 g 210 t
                                                                                                                             a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                   cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies,
                                                                                                                                                                                                                                                /tissue_type="placenta" / tissue_type="placenta" / note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site_2: ECORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LTI_NFL006_PL2"
                                                                                                                                                                                                                                                                                                                                                                       /clone="CS0DI078YB15"
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  92.0%;
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Score 18.4; DB 9; Pred. No. 1.4e+03;
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Pred. No. 1.3e+03;
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Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Siflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model,
                                                                                                 Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                         Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                894048D05.yl C. reinhardtii CC-1690, normalize
Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                          Chlamydomonadaceae; Chlamydomonas
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High quality sequence stop: 687.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 995)
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6030717839E1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163669 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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this is a NIH_MGC Library."
a 283 c 314 g 213 t
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/db_xref="taxon:9606"
/clone="IMAGE:5163669"
/clone_lib="NIH_MGC_119"
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/lab_host="DH10B"
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                                                                                                                                                                                                      GI:9210867
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.4; DB 10;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                              568 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                            Duke University
Durham, NC 27708-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
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1031062607.yl C. reinhardtii CC-1690, Stress II (normalized)
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                          Tel: 919 613 8159 Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                      DCMB Box 91000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular Plants. Project: 1031
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Contact: Elizabeth H. Harris
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                                                                                                                                                                                                 chauser@duke.edu
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/strain="CC-1690 wild type mt+
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NC 27708-1000,
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                                                                     /organism="Chlamydomonas reinhardtii"
                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZAP clones by superinfection with Exassist (Stratageme) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806.
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda zap
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94.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefeby,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chauser@duke.edu
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhOI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1590 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. POLYA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda 2AP II (Stratagene) in the EcoRI (5') and XhOI (3') sites. pBluescript II SK- plasmids were excised from the lambda
                                                                                                                                                                                                                                                                                                                       /clone_lib="C. reinhardtii CC-1690, normalized, Lambda ZapII"
                                                                                                                                                                                                                                                                                                                                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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), Lambda Zap II"
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94.7%;
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Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
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919 613 8177
                                /note="wector: pBluescript II SK-; Site_1: EcoRI; Site 2: XhoI; Stress condition II library, constructed by John Davies and Jeffrey WcDermott. combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Melis et al., (2000) plant Phys. 122: 127-135; TAP + H202 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5) and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome AS a 2006 G: 128.65."
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Chlamydomonadaceae; Chlamydomonas.
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Unpublished (2000)
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Durham, NC 27708-1000
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209 c 178 g 142 t 1 others
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Pred. No. 3.2e+03;
0; Mismatches 1;
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Search completed: November 2, Job time: 723.455 secs

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339 GCTGGGGGGCGCCTCAGCCG 321
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18; Conserv
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Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duke University
Durham, NC 27708-1000
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a 211 c 177 g 144 t 3 others
                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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## ALIGNMENTS

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RESULT 1
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                                       (UYCI-) UNIV CINCINNATI
                                                             25-NOV-1998;
                                                                                 24-NOV-1999;
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                                                                                                                            WO200031307-A1
                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an allele-specific oligonucleotide primer for the T allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5g31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T copies to higher expression of the gene. This is because the C polymorphism is found in the 5 leader sequence, which encodes a peptide c which regulates expression of the beta2AR gene. The polymorphism is c thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, migraine, anaphylaxis and chronic obstructive pulmonary disease (CODD). The gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can, therefore, be used to predict the susceptibility of an average of the gene can.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
This sequence represents the human beta2-adrenergic receptor gene, and is amplified by the primers of the invention. The primers are non-self
                                                                   Disclosure; Fig 2; 58pp; English.
                                                                                              Pairs of oligonucleotides for amplifying adrenergic receptor genes
                                                                                                                                                       WPI; 1999-327357/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta2 adrenergic receptor; genetic variation identification; hypertrophy; disease diagnosis; hypertension; prostatic disease; pulmonary disorder; asthma; peripheral vascular disorder; neuropsychic disorder;
                                                                                                                                                                                                 Buescher R,
                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                               10-NOV-1997;
                                                                                                                                                                                                                                                                                                                     04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                       W09924454-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endocrine-metabolic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlphalB-adrenergic receptor; human; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta2-adrenergic receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX61116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX61116 standard; DNA; 2300 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 2 A; 6 C; 10 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 12; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphisms in receptor (beta 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCTGGGGGGGCGTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGGGGGGGGCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                             Herrmann V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                          97us-0086232
                                                                                                                                                                                                                                                                                                                  98WO-US23496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                               Insel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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contain

primers of the invention. The primers are non-self at least 15 nucleotides (nt) and has a melting

status in an individual and to newly identified polymorphisms in the genes encoding angiotensin converting enzyme (ACE), angiotensin II receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-advenergic receptors 1 and 2. The method comprises determining the sequence at or

comprises determining the sequence at one

The invention relates to a novel method of assessing the cardiovascular

Disclosure; Page 124-125; 126pp; English.

Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern -

WPI; 2000-318010/27.

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RESULT 3
AAA38340/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                              Norberg LT, Andersson MK,
                                                                                                                                                                                                                                                             (EURO-) EURONA MEDICAL AB.
                                                                                                                                                                                                                                                                                                             14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                        20-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-adrenergic receptor-2 gene; coding region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta-adrenergic receptor-2 coding region
                                                                                                                                                                                                                                                                                              14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                          13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       W0200022166-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stroke; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA38340 standard; DNA; 2305 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               generates a homogeneous population of gene segments in a polymerase chain reaction (PCR). At least one primer in the pair can extend a 3'-end sequence complementary to a template sequence in a DNA polymerase reaction. The primers are used to amplify segments of the alphalB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular disease, hypertension and asthma, but variations may also be associated with peripheral vascular, pulmonary, neuropsychic and endocrine-metabolic disorders. These primers allow rapid and specific amplification of large and homogeneous gene segments of the alphalB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta2 adrenergic receptor genes, particularly to identify genetic variations for diagnosis of disease. Specifically variations in the alphalB gene are associated with cardiovascular disease, hypertension and prostatic disease (hypertrophy), and those in the beta2 gene with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta2 genes from a complex mixture of DNAs. This makes possible detection of genetic alterations not previously amenable to routine, automated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               large-scale sequencing analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising; anneals to two distinct segments (separated by at least 400 nt); and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        765 GGCTGGGGGGCGCCTCAGCAG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGCTGGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                            98US-0104286
98US-0104302
                                                                                                                                                                                                                                                                                                                                         99WO-IB01678
                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug screening; treatment outcome; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not previously amenable to routine, automated and
                                                                                                                                                                                                                          Lindstrom PHR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 2300;
                                                                                                                                                                                                                          Jonsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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AAZ00774/c
ID AAZ007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                  mutation
                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                      Human beta 2-adrenergic receptor DNA variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby turn decreases the duration and cost of such trials. The present sequence represents the human beta-adrenergic receptor 2 gene sequence represents the human beta-adrenergic receptor 2 gene
                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                  metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1999 (first entry)
                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ00774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen. Pragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular chey encode are useful in the screening of potential cardiovascular regimes. Determination of an individual's polymorphic nattern reduces or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ00774 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding region (GenBank Y00106/g293708). The polymorphic sites identified are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular individual cardiovascular patient. It also provides the ability to eliminate patients from clinical trials who are predicted to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGGGGGGCGCCTCAGCAG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no insert/G/C and 2070 no insert/C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                            replace(245,a)
                                                       /note= "This nucleotide differs from the wild type
                                                                                                    Location/Qualifiers replace(159,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                    nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 2
Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 2305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
30-DEC-1998;
                                                 29-JUL-1999.
                                                                                     W09937761-A1
                                                                                                                                                                              mutation
                                                                                                                                                                                                                                                      mutation
                                                                                                                                                                                                                                                                                                                            mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
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             98WO-DE03818
                                                                                                                                                                       replace(2826,g)
                                                                                                                                                                                                       /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(2078,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "This nucleotide differs from the wild type nucleic acid sequence represented in ARI00773 and results in a change in the corresponding wild type amino acid sequence from an Glu residue to Gln residue"
                                                                                                                                 /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                 replace(2640,g)
                                                                                                                                                                                                                                                                                                                       replace(2110,c)
                                                                                                                                                                                                                                                                               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(1839,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1666,c)
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(1568,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(1120,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(934,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This nucleotide differs from the wild type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                          "This nucleotide differs from the wild type
                                                                                                               nucleic acid sequence represented in AAz00773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                wild type amino acid sequence from an Ile residue to Thr residue"
                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                            nucleic acid sequence represented in AA200773"
                                                                                                                                                                                                                                                                                                                                                                      and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid sequence represented in AAZ00773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence represented in AA200773 and results in a change in the corresponding wild type amino acid sequence from an Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic
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to Arg residue"
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30-DEC-1997;

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AAZ00775/c
ID AAZ007
XX AAZ007
AC AAZ007
DT 07-OCT
XX Human |
XX Heata 2
KW Beta 2
KW neurop
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                                                                                              mutation
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                                                                                                                                                    Synthetic.
                                                                                                                                                                                                            post-traumatic stress disorder; autonomous nervous system disease;
metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                               Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                         Human beta 2-adrenergic receptor DNA variant 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ00775 standard; DNA; 3451 BP
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                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
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mining an individuals haplotype
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/note- "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773
and results in a change in the corresponding
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                                                                                    replace(1541,c)
                                                                                                        Location/Qualifiers
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Pred. No.
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RESULT 6
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                                       neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety, depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bullmia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; eating disorder; anorexia nervosa; bullmia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1559 GGCTGGGGGCGCCTCAGCAG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                 metabolic illness; gene therapy;
                                                                                                                                                   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                Human beta 2-adrenergic receptor DNA variant 4.
                                                                                                                                                                                                                                                  07-OCT-1999
                                                                                                                                                                                                                                                                                               AAZ00777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having colorium control of the system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 2a; 27pp; German
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1559 GGCTGGGGGCGCCTCAGCAG 1540
                                                                                                                                                                                                                                                                 determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including redicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develom thereasentice and/or lifectule drage.
                                                                                                                                                                             to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be
                                                                                                                                                Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 2a; 27pp; German.
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                                       1 GGCTGGGGGCGCCTCAGCAG 20
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Pred. No.
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H AAZ00778/c

AAZ00778 standard; DNA; 3451 BP

Matches Query Match

**FOCAT** 

l Similarity 20; Conserv

Conservative

0;

Mismatches

Sequence 3451 BP; 790 A; 872 C; 895 G; 894 T; 0 other;

100.0%; Score 20; DB; 100.0%; Pred. No. 8.8;

DB 20; 0;

Length 3451; Indels

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determined include neuropsychiatric disease, such as depression, anxiety, CC attention deficit disorder with hyperactivity, eating disorders, e.g. CC anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases CC of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-brager CC disposition, or migraine, allergic conditions, e.g. asthma and atopic CC disorders, and metabolic illnesses, e.g. morbid obesity including CC predicting a change in weight, using body mass index, can also be CC determined. The beta 2-adrenergic receptor sequence variants can be used CC receptor agonists can be developed. Treatments can be optimized for CC individuals, including gene therapy and pharmaceutical intervention CC individuals, including gene therapy and pharmaceutical intervention CC can developed. This sequence represents a variant of the wild type human beta varianteric receptor gene which is represented in AAZ00773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                    myocardial infarction and stroke. Other conditions that can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ00778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta 2-adrenergic receptor DNA variant 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koepke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97DE-1058401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(1541,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Timmermann B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        residue to Arg residue"
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RESULT 8
AAZOU780/c
AAZOU780/c
AAZOU79
AX AAZOU7
AX AAZOU7
AX Beta 2
KW Beta 2
KW Deurop
KW eating
KW eating
KW metabc
KW Synthe
XX Homo s
OS Synthe
XX Homo s
OS Synthe
FT Key
FT Key
FT Wutati
FT Wutati
FT Hoehe
XX WPI;
FX JOELB
XX Home
PN WO993'
XX JOER
XX Geter
XX Claim
XX Geter
XX Gene
CC Gene
CC Immun
CC This
CC Immun
CC Thor a
CC Geter
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                                                                                                                                                                  This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder, Diseases
                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta2-adrenergic receptor gene variants, useful for determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-479048/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuropyrotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; metabolic silprocas disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotector;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human beta 2-adrenergic receptor DNA variant 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ00780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1559
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the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGGGGGCGCCTCAGCAG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTGGGGGCGCCTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koepke K,
                                                                                                                                            infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97DE-1058401
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replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        b This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding and results in a change in the corresponding the corresponding and results in a change in the corresponding the corresponding to the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residue to Arg residue"
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                                                                                                                                                                                                        Claim 8; Page 12; 56pp; English.
                                                                                                                                                                                                                                                        Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaphylaxis; chronic obstructive pulmonary disease; allele-specific oligonucleotide primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; adrenergic receptor; beta2 adrenergic receptor; beta2aR; chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta
                                                                                                                                                                                                                                                                                                                                  WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-1998;
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                                                                                                                                                                                                                                             hypertension
                                                                                                                                                                                                                                                                                                                                                                                                         (UYCI-) UNIV CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200031307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta2 adrenergic receptor beta2AR C allele-specific primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA46129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA46129 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3451 BP; 789 A; 872 C; 896 G; 894 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0109886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US27963
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Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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The present sequence is an allele-specific oligonucleotide primer for the C allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide

arrhythmia, obesity, diabetes, vascular disease,

thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to be the polymorphism is

congestive heart failure, ischemic heart disease,

premature

asthma,

hypertension,

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Вb
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proteins have potential immunosuppressive, immunostimulatory, antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic, antileukemic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) class I histocompatibility antigen and/or phosphoglycerate kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
                                                                                                                                                                                                                              The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to angiopoietin, 4-hydroxybutyrate, dehydrogenese, adenosine trip osphate (ATP) dependent RNA helicase, major histocompatibility complex (MHC) class I histocompatibility antigen and/or phosphoglycerate kinase. These nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 162; 484pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic nucleic acids encoding e.g. angiopoletin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                              diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4-hydroxybutyrate; dehydrogenase; protein therapy; adenosine triphosphate-dependent RNA helicase; major histocompatibility complex Class I histocompatibility antigen; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-418297/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphoglycerate kinase; immunosuppressive; immunostimulatory;
antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic
antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single nucleotide polymorphism; SNP; angiopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA containing single nucleotide polymorphism SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH79739 standard; DNA; 51 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-2000; 2000WO-US35346.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCTGGGGGGCGCCTCAGCGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0472688
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                        modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBPs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP interaction or mRNA functionality; or RBPs that interact with the compounds. Compounds identified using the gene fragments are potentially useful for therapeutic regulation of gene expression, such as in cases of neurodegeneration, stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorders (obesity and diabetes) and bacterial or viral infection. The present sequence is one of gene fragments of the
                                                                                                                                                                                                                                  Sequences AAH27132 - AAH27151 represent human gene untranslated regions where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity. RBPs mediate the processing of pre-mRNA, the transport of mRNA from the nucleus to the cytoplasm, mRNA stabilisation, translational efficiency, and the sequestration of some mRNAs. Therefore
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 28; 33pp; English.
                            invention, isolated from the human beta-2 adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                        neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids that bind RNA-binding proteins or regulate mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-NOV-2000; 2000WO-US30888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta-2 adrenergic receptor UTR region with RBP binding ability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be used to alter phenotypic traits such as longevity, appearance, strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO20013462:-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  function, useful for therapeutic gene regulation, such as in cases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MESS-) MESSAGE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH27139 standard; DNA; 230 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGCTGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-335904/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGGGGGCGCCTCAGCGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xavier AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0437458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Query Match

Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;

92.08;

Score 18.4;

DB 22;

Length 230

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RESULT 13
AAA38784/c
           DE XX
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                                                                                                                                                                       RESULT 12
AAT93250/c
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                                                                                                                                                      Query Match
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      Human beta2 adrenergic receptor beta2AR gene
                          05-OCT-2000
                                           AAA38784;
                                                          AAA38784 standard; DNA; 2340 BP
                                                                                                                                                                                   This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251 cyanopindrol. The protein can be used in screening for agonists and antagonists, which are useful in researching asthmatic diseases.
                                                                                                                                                                  Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
                                                                                                                                                                                                                                    Disclosure; Page 27-30; 47pp; Japanese.
                                                                                                 Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases
                                                                                                                                                                                                                                                                                                                           (DAIN ) DAINIPPON PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                  P-PSDB; AAW34320
                                                                                                                                                                                                                                                                                                                                            27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                              24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                               W09735963-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-2 adrenalin receptor subtype coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthmatic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT93250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT93250 standard; cDNA to mRNA; 1999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                          1997-489627/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTGGGGGGCGCCTCAGCGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGGGGGGCGCCTCAGCAG 20
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                                                                                                                                                                                                                                                                                                           Furutani Y,
                                                                                                                                     Conservative
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                           96JP-0072914.
                                                                                                                                                                                                                                                                                                                                                            97WO-JP00982
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                                                                                                                                           92.0%;
95.0%;
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                                                                                                                                                                                                                                                                                                        Kawashima H,
                                                                                                                                     0;
                                                                                                                                           Score 18.4;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 44;
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                       Nomura A,
                                                                                                                                                  DB 18; Length 1999;
                                                                                                                                  1;
                                                                                                                                                                   0 other;
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                                                                                                                                                                                                                                                                                                       Yano K;
                                                                                                                                   Indels
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                                                                                                                                Gaps
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                                                                                                                                0,
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AAV52614/c
ID AAV52614 standard; cDNA; 3451 BP
                                             b
                                                                                                              RESULT 14
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                                                                             Matches
                                                                                             Query Match
                                          1559 GGCTGGGGGCGCCTCAGCGG 1540
                                                                                                                             determine the best treatment.
                                                                                                                                                                                                                                                        Disclosure; Figure 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                    WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                     Liggett SB;
                                                                                                                                                                                                                                                                                                                                                      (UYCI-) UNIV CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200031307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                           1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                   Local Similarity
                                                                             19;
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                     980S-0109886
                                                                                                                                                                                                                                                                                                                                                                                       99WO-US27963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1541,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1487..2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                   92.0%; Score 18.4;
95.0%; Pred. No. 44
                                                                            0,
                                                                                   Pred. No. 44;
                                                                          Mismatches
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The present sequence is a fragment of the C allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5 leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and determine the beat treatment.
                                                                                                   Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor . eta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure, hypertension -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anaphylaxis; chronic obstructive pulmonary disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; cobesity; diabetes; vascular disease; premature labour; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "beta2 adrenergic receptor"
/note= "no stop codon given at 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _leader_cistron
DB 21;
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1;

0;

Gaps

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Length 2340; Indels

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B
                                                                                                                       Matches
                                                                                        Query Match
                                                                                                                                                                                   receptor protein. Beta 2-adrenergic receptor gene alleles may be identified by any known method e.g. denaturing gel electrophoresis or PCR amplification (see also AAV52615-17). Identification preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known polymorphism in the beta 2-adrenergic receptor gene as being linked
1559 GGCTGGGGGCGCCTCAGCGG 1540
                                                                                                               Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                           to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and
                                                                                                                                                                                                                                                                                                             second alleles of the beta 2-adrenergic receptor gene, and (b) classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patients homozygous for allele encoding Arg at position 16 of
                                                                                                                                           individuals homozygous for Arg16 are more susceptible
                                                                                                                                                                                                                                                                                                                                                                        AAW75777) having an arginine residue at position 16. A novel methor identifying individuals susceptible to adverse responses to regular administration of beta agonists comprises: (a) identifying
                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA sequence codes for human beta-2-adrenergic receptor (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boushey H,
Martin RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 33-35; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta2-adrenergic receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW75777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-506372/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta-2-adrenergic receptor cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-2-adrenergic receptor; human; asthma; beta-agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1998
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                          1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                            oca1
                                                                                                                                                                                                                                                                                                                                                        genomic nucleic acid sample from the individual first and
                                                         l Similarity 95.(
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chinchilli VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "A to G substitution, results in Arg16
to Gly amino acid change"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 1588..2829
                                                                       92.0%;
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                                                                         Fred
                                                                                     Score 18.4;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fish JE,
                                                                                    DB 19;
                                                       1;
                                                       Indels
                                                                                Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ford JG;
                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                        method
                                                    Gaps
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RESULT 15
                                  attention deficit disorder with hyperactivity, eating disorders, e.g. ancrexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used
                                                                                                                                                                                   gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                          myocardial
                                                                                                                                                                                                                                                          This invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                             determined include neuropsychiatric disease, such as depression, anxiety,
                                                                                                                                                                                                                                                                                                    Claim 4; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                         determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                        Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-479048/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoehe M, Koepke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ00776 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta 2-adrenergic receptor DNA variant 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ00776;
                                                                                                                                                                      infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97DE-1058401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-DE03818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1666,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                   Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wild type amino acid sequence from an Gly residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residue to Gln residue"
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
        on:
                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
                                                                                                                                                                                                                                                                                                                Match
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/packfiles1.seq:*
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US-09-437-457-8
US-08-978-182-2
US-08-978-182-2
US-08-723-938-2
US-08-723-938-2
US-08-723-938-2
US-08-818-112-101
US-08-818-112-101
US-08-818-112-101
US-08-90-140-1
US-08-990-140-1
US-08-990-140-1
US-08-990-140-1
US-08-717-294-81
US-09-104-650-1
US-09-103-669-1
US-09-404-650-3
US-09-404-650-3
US-09-404-650-3
US-09-103-840A-2
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US-09-103-840A-1
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Sequence 1, Appli
Sequence 1, Appli
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Sequence 11, Appl
Sequence 117, Appl
Sequence 117, Appl
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Sequence 11, Appli
Sequence 1, Appli
                   Sequence 42, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
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Sequence 1,
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US-09-437-457-8/c
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                                                                                                                                                                                                                                                                                  Matches
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71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0
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US-08-118-200-1	US-07-751-891B-24	US-08-352-902D-146	US-09-199-793-1	US-08-765-192-1	US-08-270-584A-1	PCT-US95-07289-13	US-09-224-110-13	US-08-469-667-13	US-08-476-705A-3	US-09-328-111-761	US-09-056-868B-3	US-08-631-469B-3	US-09-439-313-179	US-09-030-607-179	US-09-439-313-77	US-09-030-607-77	US-09-020-956-77
		146	<u>,                                     </u>	۳.	<u>.</u>	w.	3		Sequence 3, Appli	Sequence 761, App	Sequence 3. Appli	Sequence 3, Appli	Sequence 179, App	Sequence 179, App	77,	77,	Sequence 77, Appl

## ALIGNMENTS

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; ORGANISM: Homo sapiens US-09-437-457-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Giordano, Anthony
APPLICANT: Xavier, Ashish
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES AND METHODS FOR
TITLE OF INVENTION: IDENTIFYING COMPOUNDS THAT AFFECT RNA/RNA BINDING PROTEIN
TITLE OF INVENTION: INTERACTIONS AND MRNA FUNCTIONALITY
FILE REFERENCE: 5009/014001
CUCRENT APPLICATION UNLERS: US/09/437,457
CUCRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
SEQ ID NO
SEQ ID NO
LENGTH: 230
TURNEY: NO
NUMBER OF SEX BEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08978182 Patent No. 5849556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.0%;
Best Local Similarity 95.0%;
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANN: Kaser, Matthew
APPLICANT: Mathur, Preete
TITLE OF INVENTION: HUMAN GRO
COMPUTER READABLE FORM:
                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pl
                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                          CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GGCTGGGGGGCGCCTCAGCGG 172
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                                                                                                                   E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                               Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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US-09-205-681-2/c

: Sequence 2, Application US/09205681

: Patent No. 5952214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                 ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jennir
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J
APPLICANT: Kaser, Matthew
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mathur, Preete
TITLE OF INVENTION: HUMAN GROWTH-RELATED CDC10 HOMOLOG
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LENGTH: 1926 base pairs
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LIBRARY: TLYMN
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 GGCGGTGGGCGCCTCAGCAG 242
NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                        STREET: 3174 POR CITY: Palo Alto
                                                   FILING DATE:
                                                                APPLICATION NUMBER:
                                                                                                                 FILING DATE
                                                                                                                          APPLICATION NUMBER: US/09/205,681
                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGCTGGGGGCGCCTCAGCAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                               USA
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ilarity 90.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillman, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Karl J.
                                                              08/978,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/978,182
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Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1926;
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                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                            HYPOTHETICAL: 10
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
IMMEDIATE SOURCE:
                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Coleman, Roger
TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMEDIAL: This LIBRARY: This 3003826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 GGCGGTGGGCGCCTCAGCAG 242
                                                                                                        STRANDEDNESS:
                                                                                           TOPOLOGY:
                                                                                                                                                                                        TELEX:
                                                                                                                                                                                                     TELEFAX: 415-845-4166
                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/723,938 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                      LENGTH: 1642 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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90.0%;
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                                                        Matches
                                                                                   Query Match
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                                                                                                                                                                                         MOLECULE TYPE: NO HYPOTHETICAL: NO ANTI-SENSE: NO
1228 GCTGGGGGCCCCTCATCAG 1210
                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: Consei
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                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 31, CTTY: Palo Alto
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                                                                   Local Similarity
                           2 GCTGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/080,538
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Coleman, Roger
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89.5%;
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89.5%;
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                                                               Score 15.8; DB 2;
Pred. No. 1e+02;
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0; Mismatches
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                                                  Mismatches
                                                                            Length 1642;
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                                               Gaps
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RESULT 7
US-08-818-112-101
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US-08-826-267-1
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US-08-826-267-1/c
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Patent No. 5994070
                                                                                                                                                                                                                          Sequence 101, Application US/08818112 Patent No. 6290969
                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Reed, :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8906 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                CORRESPONDENCE ADDRESS:
                               APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                     6884 GCTGGGGGCGCCGCCAG 6866
                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/014,214 FILING DATE: 27 MARCH (1996)
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17; Conserv
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                                                                                                                                                    Skeiky, Yasir A.W. Dillon, Davin C.
                                                                                                                                  Campos-Neto, Antonio
                                                                                                                                                                                           Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96, Application US/08818111 Patent No. 6338852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steel, A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C. APPLICANT: Campos-Neto, Antonia ADPLICANT: Campos-Neto, Antonia Raymond
               AUTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21(
TELECOMMUNICATION INFORMATION:
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                        STREET: U. STREET: Seattle
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Houghton, Raymond APPLICANT: Vedvick, Thomas S. APPLICANT: Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                    APPLICATION NUMBER: US/08/818,111 FILING DATE: 13-MAR-1997
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         CLASSIFICATION: 424
                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                     COUNTRY:
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Local Similarity 85.0%;
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                                                                                                                                                                                                                                                      98104-7092
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                                                                                                                                                                                                                                                                                      Washington
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                                                                                                                                                                                                                                                                                                                    6300 Columbia Center, 701 Fifth Avenue
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SYSTEM: PC-DOS/MS-DOS
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               210121.417C6
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US-09-056-556-101
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                                                         Best Local Similarity Matches 17; Conserv
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 635045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 101,
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                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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   25
                        1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                   NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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GGCCGGGGTCGCCTCCGCAG 44
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                                                                                                                                                       H: 500 base pairs nucleic acid
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                                                         Conservative
                                                                                                                                                                                                                       (206) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                   linear
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SYSTEM: PC-DOS/MS-DOS
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                                                                    76.0%;
85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.0%; Score 15.2; DB 4; 85.0%; Pred. No. 1.9e+02;
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                                                                      Score 15.2;
Pred. No. 1.
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                                                        Mismatches
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                                                                    2; DB 4;
1.9e+02;
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                                                                                  Length 500;
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                                                   Gaps
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TRE

; Sequence 1, Application US/08379496; Patent No. 5593833

RESULT 10 US-08-379-496-1

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US-08-990-140-1/c
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Olsen, Henrik S. APPLICANT: Ruben, Steven M. APPLICANT: Sonenberg, Nahum APPLICANT: Methot, Nathalie APPLICANT: Rom, Eran
                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08990140A Patent No. 6093795
                                                                                                                                                              TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) and Human TITLE OF INVENTION: etP4GF-like Protein (p97) Genes FILE REFERNCE: 1488.0700001

CURRENT APPLICATION NUMBER: US/08/990,140A

CURRENT FILING DATE: 1997-12-12

BARLIER APPLICATION NUMBER: US 60/033,151

BARLIER FILING DATE: 1996-12-13

NUMBER OF SEQ ID NOS: 13
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Best Local :
LOCATION: (97)..(2718)
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                           NAME/KEY: CDS
                                                   FEATURE:
                                                                ORGANISM: Homo sapiens
                                                                                       TYPE: DNA
                                                                                                          ENGTH: 3032
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NAME: ERNST, Batbara G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
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APPLICANT: KELLY, Paul J
TOANT: KELLY, Paul J
ASSE
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 02-MAR
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Suite 701-E, 555 13th Street.N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
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GENERAL INFORMATION:
APPLICANT: THE SC
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Best Local Similarity 85.0%;
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CURRENT FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/033,151
PRIOR FILING DATE: 1996-12-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Human Prt1-like Subunit Protein (hPrt1) Polynucleotides FILE OF INVENTION: (as amended) FILE REFERENCE: 1488.0700002
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APPLICANT:
                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME/KEY: CDS
LOCATION: (97)..(2718)
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                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE:
                                              SOFTWARE:
             APPLICATION NUMBER:
                                                                                                                                                COUNTRY:
                                                                                                                                                                             CITY: La Jolla
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10666 North Torrey Pines Road, TPC 8
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Ruben, Steven M.
Sonenberg, Nahum
Methot, Nathalie
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                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                           THE SCRIPPS RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                     The Scripps Research Institute, Office of
14-SEP-1995
                                                                                                                                                                                                                                                                                    CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING
                                                                                                                                                                                                                                                                              AND USING SAME
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            PCT/US95/11684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.2; DB 4; Length 3032; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.2; DB 3; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 81, Application US/08717294 Patent No. 6114148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
LENGTH: 105 base pairs
                                                                                REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4359 GGCTGTGGAGGCCTCAGCAG 4340
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
APPLICATION 16-SEP-1994
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 7286 base pairs
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                                                  TELEX:
                                                                                                                             NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                  TELEFAX:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 20-SE
                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
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                                                                  617-428-7045
105 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vzzeux, Rosemay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
MOLECULE TYPE:
                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 27-JAN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       FILING DATE: 26-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                     TELEFAX: (JELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ICAM-Related Materials and Methods
                         STRANDEDNESS: single
                                                TYPE: nucleic acid
                                                                                                                                                                                               NAME: No. 5837822and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/894,061 FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08 FILING DATE: 05-AUG-1994
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                           1600 base pairs
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.9e+02;
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Maximum DB seq length: 2000000000
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Perfect score:
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Match Length DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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AL553611
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BE245562
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B1911023
B1765823
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B1767868
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AV647785 AV647785
B190736 603065345
B28879 60249113
B1915042 603177231
AL553611 AL553611
B151999 603071783
BE245562 TCBAPIE21
AQ539997 RPCI-11-3
B1911023 603068746
B1765823 603047436
B1767878 6030688415
B1767878 60306093
C84644 C84644 oste
BF190014 235965 MA
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BE337782 89404805
B1722560 1031062G0
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MA/10193 ZHZ/809.S	The state of the s		n181f10	UT-H-BT0	0 518797	0	0x43a08			AW816455 OV4 - ST023	2 HS 3241	oh05c11		up02e08		BF375343 QV4-ST023	AW214864 up02e10.v	CO.	BI954411 HVSMEm001		œ				•		19349	BI527454 1024081G0

## ALIGNMENTS

W				
	FEATURES SOUTCE	JOURNAL MEDLINE COMMENT	REFERENCE AUTHORS TITLE	RESULT 1 AV647785/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Bomo sapiens" /db_xref="taxon:9606" /clone="GLCBCAO3" /clone_lib="GLC" /tissue_type="corresponding non cancerous liver tissue" /dev_stage="Adult" /lab_host="90LR" /note="Yector: pBluescript sk(-); Site_1: EcoRI; Site_2: xhoI"	Tel: 86-21-50801919(ex.45)  Fax: 86-21-50801922  Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. Location/Qualifiers 1427	with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 21625106 Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China	Hukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 427)  Xu.X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.  Insight into hepatocellular carcinogenesis at transcriptome level	

BASE COUNT

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BG284879 bs3 bp mxnn finer 602409113F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4538187 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11539 row: i column: 11
                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                   L.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                               (note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oliop-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5214802"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="leukocyte"
/lab_host="DH10B"
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Pred. No. 2.4e+02;
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Pred. No. 2.3e+02;
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI1609 row: m column: 07
                                                                                                                                                                  Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 853)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  603177231F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241774 5',
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Plate: LLAM10464 row: i column: 04
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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BG284879.1 GI:13036277
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/clone_lib="NIH_MGC_9]"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pcMv-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
a 203 c 209 g 144 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
Genoscope - Centre National de Sequencage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL553611.1 GI:12893606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL553611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 840.
Location/Qualifiers
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                                                                                                            183 a
        ilarity 100.0%; ; ; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 950)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                  /note-Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
                                                                                                  Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com"
a 291 c 262 g 210 t
                                                                                                                                                                                                                                                                                                                         /Clone="CSODIO78YB15"
/Clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site_2: ECORV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb. insert size range
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this is a NIH_MGC Library."

269 c 229 g 194 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cloning). A 0.7-3.5 kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NTH_MGC_121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5241774"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
  100.0%; Score 20; DB 9;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0;
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100.0%;
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Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                     DB 9; Length 950;
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      0,
                                                                                                  4 others
    Indels
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    0;
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Gaps
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В
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                                                                                                                                                                                           RESULT 7
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                                                               ACCESSION
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BI519989/c
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                                                                                                                                                                                                                                                  575 GGCTGGGGGCGCCTCAGCAG 556
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                                                                                                                                                                                                                                                                                          1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                     BE245562
406 bp mRNA linear EST 03-OCT-20
TCBAP1E2132 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2132, mRNA
human.
                                         BE245562.1
                                                               BE245562
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 30 High quality sequence stop: 687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 995)
NHH-MGC http://mgc.nci.nih.gov/.
NATional Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI519989 995 bp mRNA linear EST 29-AUG-20
603071783F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163669 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                             185
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 13 kb, insert size range 0.9-3 kb. Library is normalized and enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                               this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Invitrogen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:5163669"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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283 c 314 g 213 t
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                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research Genetics
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                                                                                                                                                                                                                                                                                                                                                                     Length 995;
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                                                                                                                                  EST 03-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGCTGGGGGGGCGCTCAGCAG 20
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                           RPCI-11-324D17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-324D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 \pmod{30}
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Citation: Carninci, P. and Hayashizaki, Y. High efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: clones@txccc.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1102 Bates, MC3-3320 Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schneider C, Hayashizakı r, nıyı, cırıcı çaptırapper., füll-length CDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)*

140 c 130 g 61 t 2 others
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/cell_type="pre-B cell"
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/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA"
/sex="male"
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95.0%;
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Pred. No. 9.8e+02;
""smatches 1;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                    High quality sequence stop: 643.
                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                     National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@deJong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or .rom
BACPAC Resources (http://bacpac.med.bBC end search page:
                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Class: BAC ends.
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
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/clone="IMAGE:5217922"
                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
a 112 c 141 g 89 t
                                                                                               Location/Qualifiers
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/clone_lib="RPCI-11"
/sex="Male"
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/db_xref="GDB:7624120"
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95.0%;
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DEFINITION
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High quality sequence stop: 682.
Location/Qualifiers
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Plate: LLAM11468 row: h column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 710)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                          126 a
                          /note="organ: pooled colon, kidney, stomach; Vector: pCMY-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EBORV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIHLMGC Library."
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                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5187512"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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a 209 c 189 g 134 t
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.1e+03;
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ACCESSION
                                               DEFINITION
                                                                                            BI767868/c
                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                 Matches
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COMMENT

RESULT 10 BI765823

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION

REFERENCE

TITLE

JOURNAL AUTHORS В

ORIGIN

Matches

ORIGIN BASE COUNT

VERSION

BI767868.1 GI:15759446

FEATURES

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RESULT 11
BG704787
                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
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TITLE
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        Query Match
        92.0%;
        Score 18.4;
        DB 10;

        Best Local Similarity
        95.0%;
        pred. No. 1.1e+03;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                               69 GGCTGGGGGGCGCCTCCGCAG 88
                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                              1 GGCTGGGGGGCGCCTCAGCAG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCTGGGGGGCGCCTCAGCAG 20
                             81767868 848 bp mrNA linear EST 25-SEP-2001 603060993F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5210231 5',
BI767868
                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602688415F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820931 5',
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM10726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG704787.1 GI:13978473
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                                                                                                                                                                                                                                                                                                                                                                                               179 a
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                            /note=Torgan: brain: Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIKH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

a 205 c 231 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4820931"
/clone_lib="NIH_MGC_95"
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                                                                                                                                                                                                                                                                                                92.0%;
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                                                                                                                                                                                                                                                                                                Score 18.4; DB 10;
Pred. No. 1.1e+03;
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KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
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                                                                                                                                                   JOURNAL
                                                                                                                                                                                               TITLE
                                                                                                                         MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 GACTGGGGGCGCCTCAGCAG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCTGGGGGGCGCCTCAGCAG 20
            Molecular Medicine Laboratories
Institute for Drug Discovery Research, Yamanouchi Pharmaceutica
21, Miyukigaoka, Tsukuba, Ibaraki 305, Japan
Email: kobori@yamanouchi.co.jp
                                                                                            Contact: Kobori M
                                                                                                                           method involving the preparation of a subtracted cDNA library Genes Cells 3 (7), 459-475 (1998)
                                                                                                                                                                                                                Kobori,M., Ikeda,Y., Nara,H., Kato,M., Kumegawa,M., Nojima,H. and
                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                               C84644 161 bp mRNA linear EST 26-MAR-1
C84644 osteoclast subtracted library Oryctolagus cuniculus cDNA,
                                                                                                                      98424349
                                                                                                                                                                  Large scale isolation of osteoclast specific genes by an improved
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 161)
                                                                                                                                                                                                                                                                                                                                                                                                 C84644.1 GI:4527904
                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                        rabbit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLAM11527 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled lung and spleen; Vector: pCNV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

265 c 230 g 195 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:5210231"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 1.1e+03;
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1 GGCTGGGGGGCGCCTCAGCA 19

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ORIGIN
                                                                                                BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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           Matches
                             Best
                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GCTGGGGGGCGCCTCAGCA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GCTGGGGGCGCCTCAGCA 19
                                                                                                                                                                                                                                                                                      Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235965 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence BF190014
                                                                                                                                                                                                                                                                                                   Plate: 60 row: A column: 6
                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 132) Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stone, R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF190014.1 GI:11073383
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                                                                                                                                                                                                                                                                                                                                                                              -minmatch 12 options.
         Conservative
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                                                                                         /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 36 c 45 g 19 t
                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                 /clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="osteoclast subtracted library"
/tissue_rype="long bone"
/cell_type="osteoclast"
/cell_line="primary"
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52 c 36 g
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                  87.0%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (2000)
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                Score 17.4; DB 10;
Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Pred. No.
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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Search completed: November 2, 2002, 17:57:24 Job time: 721.455 secs
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KEYWORDS
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                                                                                                                                                                Matches
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                                                                                                                                                                                   Best Local Similarity
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                                                                               312 GGCTGGGGACGCCTCAGCA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                      1 GGCTGGGGGGCGCCTCAGCA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 355)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA840344 355 bp mRNA linear EST 27-FEB-1998 ww92a05.il Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1262384 5' similar to TR:Q14467 Q14467 MRNA; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28m13 rev1 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:664936
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                                                                                                                                                                                                                                                              81
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouseest@watson.wustl.edu
                                                                                                                                                                                                                                         /strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1262384"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole skin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                             87.0%;
94.7%;
                                                                                                                                                            0,
                                                                                                                                                                           Score 17.4; DB 9; Length 355; Pred. No. 2.4e+03;
                                                                                                                                                          Mismatches
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
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Result No.

Query Score Match Length DB

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Description

SUMMARIES

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ion		Pate	Shim			Sequence AX204241			16.8	16.8	16.8	16.8	16.8	0 00 0	200	16.8	16.8	16.8 16.8	17 16.8	17.4	17.4 17.4	18 17.4	18.4 18	18.4	18.4	18.4	18.4	20	20	200	20	20 20	20
/db_x 26 /note	Location/Qualifier 151 /organism="Homo sa	mt: WO (	kets, R. A	י א פכ	14248.1	lence 354	) )		84.0 2	84.0 1	84.0 1	84.0 1 84.0 1	84.0 1	84.0	84.0	84.0	84.0	84.0 84.0	85.0 84.0	87.0 1 87.0 2	87.0 87.0	90.0 1 87.0	92.0 90.0 1	92.0	92.0	92.0	2.0	100.0 1	0.0		0.00	0.0	0.0
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ıism			polymorphisms and	ertebrata; Euteleostomi; Hominidae; Homo.		linear PAT 30-AUG-2001			AC102955 Rattus no	AC077693 Oryza sat	AC105872 Rattus no	AC095200 Rattus no AC084831 Oryza sat	AC094467 Rattus no AC006001 Homo sapi	AC105963 Mus muscu	X59734 X.laevis 28	AB022919 Rhodopseu	L08777 Chlorobium	AJ279460 Unidentif	AC099942 Mus muscu K01371 X.laevis oo	AC015559 Homo sapi AL662911 Mus muscu	AC094344 Rattus no AL354677 Homo sapi	AL590464 Streptomy AC109752 Rattus no	J02960 Human beta- AL590463 Streptomy	AX022521 Sequence AX022523 Sequence	AX022518 Sequence AX022520 Sequence	AX022517 Sequence	BC012481 Homo sapi	AC011354 Homo sapi	AX334116 Sequence M15169 Human beta-	AX022522 Sequence AX332732 Sequence	AX022519 Sequence	AR164456 Sequence	AX204248 Sequence

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87105974
                                                                                       Data
                                                                                                                                                                                                               Cloning and sequence analysis of the human brain beta adrenergic receptor. Evolutionary relationship to rodent and avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 230) McAllen,J. III, Overaker,D.W. and Cooper,K.L. Absorbable rivet/pin applier for use in surgical procedures Patent: US 6273893-A 8 14-AUG-2001;
                                                                                                substantial corrections are reported in [2]
                                                                                                                   Submitted (22-SEP-1987)
                                                                                                                                                                                                 beta-receptors and porcine muscarinic receptors
                                                                                                                                                                                                                                              Chung, F.Z., Lentes, K.U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                           Human mRNA for brain beta-adrenergic receptor.
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                                                                                                                                              Kerlavage,A.R.
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/clone_lib="neonatal human 178. .1419
                           /db_xref="taxon:9606"
                                       /organism="Homo sapiens"
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                                                                   Location/Qualifiers
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1 91 c 70 g
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                                                                 20;
                                                                                                                                                                                                                                                                                              1 (bases 1 to 3451)
Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                Patent: WO 9937761-A 3 29-JUL-1999;
HOEHE MARGRET (DE); KOEPKE KARLA (DE);
                                                                                                                                                                                                                                                                                   and use thereof
                                                                                                                                                                                                                                                                                                                                                                      unidentified
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Sequence 3 from Patent W09937761.
AX022519
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1491, .1496
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                                                                                                                                                               /organism="unidentified"
/db_xref="taxon:32644"
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508 c 482 g
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LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMMTFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVMIV
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Ilmgtftlcmlpffivnivhviqdnlirkevyillnmigyvnsgfnpliycrspdfri
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/protein_id="CAA28511.1"
/db_xref="GI:29373"
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                                                                               100.0%;
                                                                                                                                                   872 c
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                                                                                                                                              897 g
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                                                                             Score 20; DB 6;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 9;
Pred. No. 1.3e+02;
                                                               Mismatches
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DEFINITION
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                                                                                                                                        1 CCCCGCCGTGGGTCCGCCCG 20
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                                                                                                               CCCCGCCGTGGGTCCGCCCG 1542
                                                                                                                                                                      20;
      AX334116.1 GI:18124835
                       Sequence 4625 from Patent AX334116
                                               AX334116
                                                                                                                                                                                                                                                                                                                                   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                      Avaion Pharmaceuticals (US)
                                                                                                                                                                                                                                                                                                                                  gene sets
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX332732.1 GI:18123366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3241 from Patent W00194629.
                                                                                                                                                                                                                                                                                                                     Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX332732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOEHE MARGRET (DE); KOEPKE KARLA (DE);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 9937761-A 6 29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 3451)
Hoche, M., Koepke, K. and Timmermann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6 from Patent W09937761.
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873 c 895 g
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1. .3451
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                                                                                                                                                                                                                                                              /organism≈"Homo sapiens"
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873 c 897 g
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Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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                                           PAT 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                          cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dixon,R.A., Keller,P., Caron,M.G. and Lefkowitz,R.J. belineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Lefkowitz, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robilka,B.K., Dixon,R.A., Frielle,T., Dohlman,H.G.,
Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U., Caron,M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 3451)

Kobilka, B.K., Frielle, T., Dohlman, H.G., Bolanowski, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87222338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adrenergic receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M15169 J02728 M16106
M15169.1 GI:178201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta-2-adrenergic receptor mRNA, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avalon Pharmaceuticals (US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1399 to 1985)
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                           1369...3383
/gene="ADRB2"
1376...3383
/gene="ADRB2"
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/note="b-2-adr mRNA (alt.); G00-120-541"
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                                                                                                      /note="b-2-adr mRNA (alt.); G00-120-541"
                                                                                                                                                        1369.
                                                                                                                                                                       /tissue_type="placenta"
/tissue_lib="Evan Sadler"
                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/map="5q31-q32"
                                                                                                                              /gene="ADRB2"
                                                                                                                                                                                                                  /clone=
                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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873 c 895 g
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                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A. 84 (1), 46-50 (1987)
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Pred. No. 1.1e+02;
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                                                                                                                        Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 27, 2001 this sequence version replaced gi:13699555.
    www-shgc_stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
                                                                                                                                                                                                                               Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 133042)
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DOE Joint Genome Institute and Stanford Human Genome Center
Direct Submission
Estimated Total Number of Errors is 0.1
                                                            Finishing Completed at Stanford Human Genome Center
                                                                                                  Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                             DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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/translation="MGQPENGSAFILAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
/translation="MGQPENGSAFILAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV
LAIVFGNVLVTTA1KFFERLQTVTNYFITSLACADLVMGLAVVPFGAHILMKWMTFG
NFWCDEWTSLDVLCVTASIETLCVLAVDRYFA1FSPFKYOSLJTKNKAPKFILMVWTV
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYALASSLVSFYVDLVLMVFV
YSRVFQEAKRQLOKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="beta-2 adrenergic receptor"
/protein_id="AAAA88015.1"
/db_xref="GI:178202"
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/db_xref="GI:560761"
/db_xref="GB:560761"
/db_xref="GB:500761"
/translation="MRLPGVRSRPAEPRRGSAR"
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RESULT 11
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Best Local Similarity
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Submitted (27-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On NOV 27, 2001 this sequence version replaced gi:12830127.
                                                                                                                                                                                                                                                                                                                                                            Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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                                                                                                                                                                                                                                                                                                                                                                                                    www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                         www.jgi.doe.gov
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/chromosome="5"
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/db_xref="taxon:9606"
/chromosome="5"
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DEFINITION

BC012481

HOMO sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds.

2063 bp

mRNA

linear

PRI 20-AUG-2001

ACCESSION

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                DEFINITION
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KEYWORDS
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                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                              1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                   CCCCGCCGTGGGTCCGCCTG 176
    Human gene for beta-adrenergic receptor (beta-2 subtype)
                                      HSBAR
                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/TLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: k Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 178203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., G
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAIVEGNVLVITAIAKFERLQTVTNYEITSLACADLVNGLAVVPEGAAHILMKMMTEG
NEWCEEWTSIDVLCVTASIETLCVIAVDRYFAITSPEKYQSLLTKNKARVIILMVMIV
SGLTSELPIQMHMYRATHQEAINCYANETCCDEFTNQAYALASSIVSEYVPLVIMVEV
                                                                                                                                                                                                                                                                                                                                                                                   TVPSDNIDSPGRNCSTNDSLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAH12481.1"
/db_xref="GI:15214694"
/translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                                                                                                                                                                                                                                                                                                                                                                                                                       IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:21367 IMAGE:4538187"
/tissue_type="Prostate, adenocarcinoma."
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Pred. No. 6e+02;
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3451 bp
Sequence 1 from Patent W09937761.
AX022517
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Submitted (20-OCT-1987)
                                                                                                                                                                                                                       Similarity
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Y00106.1 GI:29370
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Nucleic Acids Res. 15 (8), 3636 (1987)
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                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                   /note="membrane spanning domain VI" 1712. .1774
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFUELLCLERSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGQPGNGSAFLLAPNRSHAPDHDVTQQRDEVWVVGNGIVNSLIV
LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVNGLAVVPFGAAHILMKMWTFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMKWWIV
SGLTSFLDIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/db_xref="GI:29371"
                                                                                                                                                                                                                                                                                                                                                                                   note="membrane spanning domain v"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="membrane spanning domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="membrane spanning domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="membrane spanning domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                      'note="membrane spanning domain IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="N-linked glycosylation site"
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                                DNA
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AX022517.1 GI:10046115

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SOURCE
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       1 (bases 1 to 3451)
Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                        19;
and use thereof
                                                                        unidentified
                                                                                     unidentified
                                                                                                                  AX022520.1 GI:10046119
                                                                                                                               Sequence 4 from Patent WO9937761. AX022520
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Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
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Sequence 2 from Patent WO9937761.
AX022518
                                                          unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                            HOBHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 9937761-A 2 29-JUL-1999;
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HOBHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
MOLEKULA (DE); TIMMERNANN BERND (DE)
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Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and use thereof
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                                                                                                                                                                                                                                                                                                                                                       /organism="unidentified"
/db_xref="taxon:32644"
872 c 895 g 89
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/db_xref="taxon:32644"
871 c 892 g 894
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Pred: No. 5.3e+02;
                                                                                                                                                         3451 bp
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source
                                                        Local Similarity
                                                                                                                                                      Patent: WO 9937761-A 4 29-JUL-1999;
HOEHE MARGRET (DE); KOEFKE KARLA (DE); MAX DELBRUECK CT FUER
MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                      789 a
                                              Conservative
                                                                                                  /db_xref="taxon:32644"
872 c 896 g
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1. .3451
                                                                                                                          organism="unidentified"
                                                     92.0%;
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Search completed: November 2, 2002, 16:50:24 Job time: 416.636 secs

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Database :
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AJ312 L0560 U2316 AJ312

## ALIGNMENTS

COMMENT REMARK JOURNAL TITLE AUTHORS NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds. EC012481
EC012481.1 GI:15214693 Tissue Procurement: DCTD/DTP Strausberg, R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens BC012481 numan. (bases 1 to 2063) 2063 bp mRNA linear PRI 20-AUG-2001

Result

No.

Query Score Match Length DB

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Description

SUMMARIES

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTGGGGGGCGCCTCAGCAG 174
                                                        Direct Submission
Submitted (20-OCT-1987)
                                                                                                    Schofield, P.R.
                                                                                                                                                 1 (bases 1 to 2305)
Schofield, P.R., Rhee, L.M. and Peralta, E.G.
Primary structure of the human beta-adrenergic receptor gene
Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                          beta-adrenergic receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garc:
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 28 Row: k Column: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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                                                                                                                        (bases 1 to 2305)
                                                                                                                                                                                                                                                                                                                                                                                              gene for beta-adrenergic receptor (beta-2 subtype).
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                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     GI:29370
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TVPSSNIDSPGRNCSTNDSLL"
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YSRVEOEAKROLOKIDKSEGRFHYONLSOVEQDGRTGHGLRRSSKFCLKEHKALKYLG
IIMGTFTLCWLPFFIVNIVHVIQDNLLKKEYYILLNWIGYVNSGENPLIYCRSPDFRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surface"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Similar to adrenergic, beta-2-, receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="MGC:21367 IMAGE:4538187"
/tlssue_type="Prostate, adenocarcinoma."
/clone_lib="NHH MGC_91"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=:
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
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HSBAR/c RESULT 2 Locus

FEATURES

100.0%;

Score 20;

DB

Length 3451;

REFERENCE

TITLE JOURNAL AUTHORS MEDLINE REFERENCE

TITLE

JOURNAL AUTHORS SOURCE

KEYWORDS VERSION

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765 GGCTGGGGGCGCCTCAGCAG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                           Patent: WO 9937761-A 1 29-JUL-1999;
HOEHE MARGRET (DE); KOEPKE KARLA (DE
MOLEKULA (DE); TIMMERWANN BERND (DE)
                                                                                                                                                                                                                            1 (bases 1 to 3451)
Hoehe, M., Koepke, K. and Timmermann, B.
                                                                                                                                                                                                 Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                       unclassified.
                                                                                                                                                                                                                                                                                                               unidentified
                                                                                                                                                                                                                                                                                                                                   unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1 from Patent W09937761. AX022517
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/db_xref="taxon:32644"
871 c 892 g
                                                                           Location/Qualifiers
1. .3451
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1712. 1774
/note="membrane spanning domain VII"
a 616 c 649 g 545 t
                                                 /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="membrane spanning domain IV" 1385. .1450
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1114. .1180
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NEWCEFWISIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
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/clone_lib="Maniatis human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="N-linked glycosylation site"
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/db_xref="taxon:9606"
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                       GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                       HOEHE MARGRET (DE); KOEPKE KARLA (DE); MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                                                                  and use
                                                                                                                                                                                                                                                                                                                                 Sequence 4 from Patent WO9937761 Ax022520
                                                                                                                                                                                                   Patent: WO 9937761-A 4 29-JUL-1999;
                                                                                                                                                                                                                    Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                               unidentified
                                                                                                                                                                                                                                                                                                                   AX022520.1
                                                              Similarity
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Novel sequence variants of the human beta2-adrenergic receptor gene
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/db_xref="taxon:32644"
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                     Human beta-2-adrenergic receptor gene, complete cds
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J02960.1 GI:178203
              J02960
                                       HUMADRBRA
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Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                           unidentified
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Sequence 5 from Patent W09937761
AX022521
                                                                                                                                                                                                                                                                                              MOLEKULA (DE); TIMMERMANN BERND (DE)
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                                                                                                                                                                                                                                                                                                                                                                                             unclassified
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Novel sequence variants of the human beta2-adrenergic receptor gene
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    Sequence
AX204248
                                                                                                                                                                                                                                                                                                                                             777 a 890 c 886 g 905 t
1 bp upstream of EcoRI site; chromosome 5q31-q32.
                                                   AX204248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Durieu-Trautmann,O. and Strosberg,A.D. Structure of the gene for human beta 2-adrenergic receptor: expression and promoter characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88041037
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Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis DNA.
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                 354 from Patent W00148245.
                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xeef="5DB:600-120-541"

/db_xeef="5DB:600-120-541"

/translation="MGQPGNGSAFILAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
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SGLTSFLPIQMHWYRATHQEAINCYANETCCDFTNQAYALASSIVSFYPLVIMYFY
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INGTETLCULPFEIVNIVHVIQDNLIRKEVVILLANGTVNSGFWRDLIYCRSPDERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRVFTFCVCHHVFVLLGASVFVSGRVSYLDRGDFVPDGFCVBARASVHVGELGGCVSV
SMAVVRKSEHVCQGVFVPVCACLGGHSRFLFNVGQCRCAALCLETSSRAGAQGRQVA
ATEEPKAPGLAGKHTTSSFSPLGFARVAGKOWWPALQCAVGPRPGQPQEKEGEGRGGK
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/protein_id="AAA88016.1"
/db_xref="G1:560762"
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/cell_line="A431"
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/map="5q31-q32"
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Chung, F. Z., Lentes, K.U., Gocayne, J., Fitzgerald, M., Robinson, D.,
                                                                    Homo sapiens
                                                   Eukaryota;
                                         Mammalia;
                                                                                              beta-adrenergic receptor.
                                                                                                               X04827.1 GI:29372
                                                                                                                                    Human mRNA for brain beta-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                              Absorbable rivet/pin applier for use in surgical procedures Patent: US 6273893\text{-A} 8 14\text{-AUG-}2001;
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                                                                                                                                                           HSBARR
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McAllen, J. III, Overaker, D.W. and Cooper, K.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 from patent US 6273893. AR164456
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                      Maryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1970)
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Patent: WO 0148245-A 354 05-JUL-2001;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                          1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                                             19;
 Patent: WO 9937761-A 3 29-JUL-1999;
HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
                                            Novel sequence variants of the human beta2-adrenergic receptor gene and use thereof
                                                                        Hoehe, M., Koepke, K. and Timmermann, B
                                                                                                                             unidentified
                                                                                                                                                                                         3451 bp
Sequence 3 from Patent WO9937761.
AX022519
                                                                                                                                           unidentified
                                                                                                                                                                        AX022519.1 GI:10046118
                                                                                                            unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substantial corrections are reported in [2] Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kerlavage,A.R., Fraser,C.M. and Venter,J.C. Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (22-SEP-1987)
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                                                                                       (bases 1 to 3451)
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1502. .1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT: P07550"
/translation="mgQpgngsafllapngshapdhdvTQerdevwyvgmgivmsliv_laivegnvlvItalakferlQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFGNFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="polyA site"
508 c 482 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pot. polyA signal"
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1491. .1496
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA28511.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="beta-adrenergic receptor (AA 1-413)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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95.0%;
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Pred. No. 1.
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1559 GGCTGGGGGGCGCCTCAGCGG 1540
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                                                                                                                                                        Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
                                                                                                                                                                                                                                                                                                                        Sequence 3241 from Patent W00194629
AX332732
                                                                                                          Patent:
                                                                                                                            gene sets
                                                                                                                                Horrigan, S., Soppet, D.R. and Weaver, \mathbf{Z}. Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                        Avalon Pharmaceuticals
                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                           AX332732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOEHE MARGRET (DE); KOEPKE KARLA (DE MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: WO 9937761-A 6 29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel sequence variants of the human beta2-adrenergic receptor gene
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                                                                                                      WO 0194629-A 3241 13-DEC-2001;
                    /db_xref="taxon:9606"
                                  /organism="Homo sapiens"
                                                                dimaceuticals (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/db_xref="taxon:32644"
873 c 897 g 89;
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Pred. No. 1.1e+02;
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Search completed: November 2, 2002, 16:51:07 Job time: 390.636 secs
                                                                   Db 1559 GGCTGGGGGCGCCTCAGCGG 1540
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AX334116/c
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                                                                                                                                   Query Match 92.0%; Score 18.4; DB 6; Length 3451; Best Local Similarity 95.0%; Pred. No. 1.1e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                         source
                                                                                                     1 GGCTGGGGGGCGCCTCAGCAG 20
                                                                                                                                                                                                                                                                                                                                                               Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Sequence 4625 from Patent WO0194629,
AX334116
                                                                                                                                                                                                                                                                                     Patent: Wo 0194629-A 4625 13-DEC-2001;
Avaion Pharmaceuticals (US)
Coation/Qualifiers
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/db_xref="taxon:9606"
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                          o.
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                               Score
                            Match Length DB
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                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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20
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                     Description
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AX204248/c
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                                                                                              Shimkets,R.A. and Leach,M.

Nucleic acids containing single nucleotide polymorphisms
methods of use thereof
Patent: WO 0148245-A 354 05-JUL-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                        51 bp
Sequence 354 from Patent W00148245.
AX204248
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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26
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X71874 H.sapiens g AL032819 Homo sapi AC100762 Homo sapi

PAT 30-AUG-2001

BC000099 Homo sapi AY046538 Homo sapi AF006751 Homo sapi AB037819 Homo sapi

M96584

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AX337830 Sequence AX014224 Sequence

AC107312 Homo sapi AC017090 Homo sapi AJ323085 Homo sapi

AC011299 Homo sapi AC022566 Homo sapi

AC080050 Homo sapi AC020598 Homo sapi AC012486 Homo sapi AC0124171 Homo sapi AC092171 Homo sapi AC0921861 Homo sapi AC090865 Homo sapi AL133419 Human DNA

Y00106 Human gene AX022517 Sequence AX022518 Sequence AX022520 Sequence AX022521 Sequence AX022521 Sequence AX022523 Sequence AX022523 Sequence AX022523 Sequence AX022521 Human beta-AC012615 Homo sapi AF217204 Canis fam

X04827 Human mRNA
AX022519 Sequence
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AX32732 Sequence
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AX33116 Sequence
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AC011354 Homo sapi
AC012635 Homo sapi
AC027635 Homo sapi

AX204248 Sequence AR164456 Sequence

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                                                                                      substantial corrections are reported in [2] Data Kindly reviewed (22 SEP-1987) by Kerlavage A.R.
                                                                                                                      Submitted (22-SEP-1987)
                                                                                                                                          Direct Submission
                                                                                                                                                       2 (bases 1 to 1970)
Kerlavage, A.R.
                                                                                                                                                                                             beta-receptors and porcine muscarinic receptors FEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                       87105974
                                                                                                                                                                                                                                    receptor.
                                                                                                                                                                                                                                                                                                                                                                                           X04827.1 GI:29372
                                                                                                                                                                                                                                                                                                                                                                                                             X04827
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                                                                            Location/Qualifiers
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                                  1 GGCTGGGGGGCGCCTCAGCGG 20
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20; Conser
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Novel sequence variants of the human beta2-adrenergic receptor gene
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Sequence 3 from Patent WO9937761.
                                                                                                                                                                                                                                                HOBHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER MOLEKULA (DE); TIMMERMANN BERND (DE)
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                                                                      Conservative
                                                                                                                                                          /db_xref="taxon:32644"
872 c 897 g
                                                                                                                                                                                              /organism="unidentified"
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508 c 482 g
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/db_xref="Swiss-prot: P07550"
/translation="MGOPGNGSAFLLAPNGSHAPDHDVTQERDEVWVVGWGIVWSLIV
LATVEGNVLVITALAKEERLOGVTNVFITSLACADLVNGLAVVEPGAHILMKMWIFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKMARVILLWMWIV
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YSRVFQEAKRQLQXIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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1952. .1957
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965. .970
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/db_xref="GI:29373"
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                                                                                   100.0%; Score 20; 100.0%; Pred. No.
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                     AX334116 3451 bp E
Sequence 4625 from Patent W00194629.
AX334116
        AX334116.1 GI:18124835
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                                                                                                                                                                                                                                                                                                                             Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                               Avalon Pharmaceuticals (US)
                                                                                                                                                                                                                                                                                                                           gene sets
                                                                                                                                                                                                                                                                                                                                              Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
MOLEKULA (DE); TIMMERNANN BERND (DE)
                                                                                                                                                                                                                                                                                                                 Patent:
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Hoehe, M., Koepke, K. and Timmermann, B.
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873 c 895 g
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1559 GGCTGGGGGGCCTCAGCGG 1540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Lefkowitz,R.J. cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kobilka, B.K., Dixon, R.A., Frielle, T., Dohlman, H.G.,
Bolanowski, M.A., Sigal, 1.S., Yang-Feng, T.L., Francke, U., Caron, M.G.
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Kobilka, B.K., Frielle, T., Dohlman, H.G., Bolanowski, M.A.,
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Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
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                                                                                                           /note="b-2-adr mRNA (alt.); G00-120-541"
1369. .3383
                                                                                                                                                          /gene="ADRB2"
                                                                                                                                                                                                               /tissue_type="placenta"
/tissue_lib="Evan Sadler"
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/gene="ADRB2"
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                                                                                                 Submitted (27-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 27, 2001 this sequence version replaced gi:13699555. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: Phrap Quality >=40 99.9% of Sequence: Estimated Total Number of Errors is 0.1.
                                             Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                        www.jgi.doe.gov
                                                                                                                                                                                               Direct Submission
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LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKWWTEG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
SGLTSFLPIQMHWYRATHQBAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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/protein_id="AAA88015.1"
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/db_xref="GDB:G00-120-541"
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DEFINITION **FOCUS** 

AC027635

AC027635 142239 bp DNA 1 Homo sapiens chromosome 3 clone RP11-571C11, PROGRESS \*\*\*, 60 unordered pieces.

linear

HTG 01-SEP-2000

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                     Finishing Completed at Stanford Human Genome Center
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/clone="CTC-235N17"
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Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 1100609 bases at least 040
Consensus quality: 115224 bases at least 030
Consensus quality: 113413 bases at least 020
Insert size: 138700; squrose-fp
Insert size: 135700; squrose-fp
Ouality coverage: 1.74 in 020 bases; squrose-fp
Ouality coverage: 2.65 in 020 bases; squrose-fp
Ouality coverage: 2.65 in 020 bases; squrose-fp
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Summary Statistics
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On Sep 1, 2000 this sequence version replaced qi:7658491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston, R.H.
Direct Submission
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Waterston, R.H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                          1 GGCTGGGGGGCGCCTCAGCG 19
                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                           19;
                                                                                             Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds. BC012481
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      Homo sapiens
                                                                              BC012481.1 GI:15214693
                                                                                                                                         BC012481
                                                    numan
                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig97"
18548. .19671
                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig96"
17040. .18447
                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig95"
15140. .16939
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig93"
13391. .15039
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig90"
12015. .13290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig84"
8021. .9089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-571C11"
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13649: contig of 3237 k
133749: gap of unknown 1
137465: contig of 3716 k
137565: gap of unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122841: gap of 1
126444: contig of 1
126544: gap of 1
130312: contig
                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 2; 100.0%; Pred. No. 1.2e+(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142239: contig of 974 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141265: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137565: gap of unknown length
141165: contig of 3600 bp in length
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111408:
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                                                                                                                                      2063 bp
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of 3768
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of 3723
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of 3478
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                        1 GGCTGGGGGCGCCTCAGCGG 20
                                                                                                                                                                    HSBAR 2305 bp DNA linear PRI 1 Human gene for beta-adrenergic receptor (beta-2 subtype).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: k Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 178203.
  Eukaryota;
                             Homo sapiens
                                                                                beta-adrenergic receptor.
                                                                                                                       Y00106.1 GI:29370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: villalon@bom.tmc.edu.

Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,

N.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2063)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 a
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IIMGTFTLCWLPEFIVNIYHYIQDNLIRKEYYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFYGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAIVEGNVLVITAIAKEERLQTVTNYFITSLACADLVMGLAVVPEGAAHILMKMATEG
NEWCSEWTSIDVLCVTASIETLCVIAVDRYFAITSPEKYQSLLTKNKARVIILMVWIV
SGLTSELPIQMHWYRATHQEAINCYANETCCDEFTNQAYAIASSIVSEYVPLVIMVFV
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/db_xref="G1:15214694"
/translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Similar to adrenergic, beta-2-, receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
222. .1463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Prostate,
/clone_lib="NIH_MGC_91"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MGC:21367 IMAGE:4538187"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 c
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95.0%;
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Pred. No. 4.1e+02;
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DEFINITION ACCESSION
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AUTHORS
TITLE
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                                                                                                                                                                                                                                             RESULT 14
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         unclassified.

1 (bases 1 to 3451)

Hoehe,M., Koepke,K. and Timmermann,B.

Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                  Sequence 1 from Patent W09937761. AX022517
                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
19; Conserv
and use thereof
                                                                                            unidentified
                                                                                                              unidentified
                                                                                                                                                AX022517.1 GI:10046115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-OCT-1987)
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Schofield, P.R., Rhee, L.M. and Peralta, E.G.
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/note="membrane spanning domain VII"
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HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                                                                                              1 (bases 1 to 3451)
Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
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HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERWANN BERND (DE)
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2 from Patent W09937761.
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Copyright (c) 1993 - 2002 Compugen Ltd
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Sequence 27 from Patent WO9735973.
A65746
                                                                                                                      Other publication FR 2746813 19971003
                                                                                                                                            Strosberg,A.D.
CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF Patent: WO 9735973-A 27 02-OCT-1997;
VETIGEN (FR)
                                                                                                                                                                                                                                                                                          unidentified
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Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and
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AE005005 Halobacte
AE005887 Caulobact
AE002033 Deinococc
AE008064 Agrobacte
AE009099 Agrobacte
AE007072 Mycobacte
AE007072 Mycobacte
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AB005756 Homo sapi
AB006755 Homo sapi
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M25858 Human von W
AR065637 Sequence
AR096665 Sequence
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AX022519 Sequence
AX022522 Sequence
AX332732 Sequence
AX334116 Sequence
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AL021184 Mycobacte
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X04385 Human mRNA
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AC095021 Sus scrof
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AC011334 Homo sapi
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AC018327 Drosophil
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X04827 Human mRNA
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AR164456 Sequence
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                                                                                                                                                           1 (bases 1 to 230)
McAllen,J. III, Overaker,D.W. and Cooper,K.L.
Absorbable rivet/pin applier for use in surgical procedures
Patent: US 6273893-A 8 14-AUG-2001;
                                                                                                                                                                                                                                 Unknown.
                                                                                                                                                                                                                                                                                 Sequence 8 from patent US 6273893. AR164456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                   Unclassified.
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Ax204248
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                                                  Conservative
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                                                                                                                /organism="unknown"
91 c 70 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="single nucleotide polymorphism Accession number cg43040273"
                                                                                                                                                   Location/Qualifiers
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                                                          100.0%; Score 15; DB 6; 100.0%; Pred. No. 8.8e+02;
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                                             1 (bases 1 to 1970)
Chung.F.Z., Lentes,K.U., Gocayne,J., Fitzgerald,M., Robinson,D.,
Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
Cloning and sequence analysis of the human brain beta-adrenergic
receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors
                                                                                                                                                                                                                                                                                                               X04827
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                    beta-adrenergic receptor.
                                                                                                                                                                                                                                                                                 X04827.1 GI:29372
                                                                                                                                                                                                                                                                                                                               Human mRNA for brain beta-adrenergic receptor.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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297A, Baltimore Maryland 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-DEC-1995) C.W. Emala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1948)
Emala, C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Anim. Sci. 74 (9), 97034778
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LAIVVGNVLVITA LARFERLQTVINYFITSLARAFVLTAKKARVVLLMKMMTFG
NEWCEFWTS.DVLCVTAS.BETLCVIAURIV
SGLTSELPIQMHWYRATHQEAINCYAKETCCDFFTNQAYAIASSIVSFYLPLVMWIV
SGLTSELPIQMHWYRATHQEAINCYAKETCCDFFTNQAYAIASSIVSFYLPLVMWIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="beta2-adrenergic receptor"
/protein_id="CAA64316.1"
/db_xref="GI:1359589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIMGTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLNWVGYVNSAFNPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="cardiac muscle"
151. .1398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Canis familiaris"
/db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 15; DB 4; 100.0%; Pred. No. 7.8e+02;
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RESULT 6
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Best Local Similarity
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                                                                                                Strosberg, A.D.

CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF Patent: WO 9735973-A 1 02-0CT-1997;
                                                                                                                                                                                                                                                                               Sequence 1 from Patent W09735973.
                                                                                                                                             Lenzen, G., Pietri-Rouxel, F., Drumare, Marie-Francoise and
                                                                                                                                                                                                              unidentified
                                                                                      VETIGEN (FR)
                                                                                                                                                                                          unclassified
                                                                                                                                                                                                                              unidentified.
                                                                                                                                                                                                                                                           A65720.1 GI:4531340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substantial corrections are reported in [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-SEP-1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kerlavage, A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 211 (2), 200-206 (1987) 87105974
                                                                                                                                                                      (bases 1 to 2679)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 a
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                                                                 publication FR 2746813 19971003.
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l. .26/5
/organism="unidentified"
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="polyA site"
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YSRVEQEAKROLOKIDKSEGRFHVONLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNLYHVIQDNLLIRKEYVILLNWIGYVNSGENPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="pot. polyA signal"
1970
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1952. .1957
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NEWCEEWTSIDVLCVTASIETLCVIAVDRXEAITSPEKXQSLLTKNKARVIILMVMIV
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/translation="MGQPGNGSAFLLAPNGSHAPDHDVTQERDEVWVVGMGIVMSLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA28511.1"
/db_xref="GI:29373"
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178. .1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="beta-adrenergic receptor (AA 1-413)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 15; DB 9; 100.0%; Pred. No. 7.8e+02;
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ORIGIN
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AX022522
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AX022519
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Query Match
Best Local Similarity
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                                                                                                                    HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                        Hoehe,M., Koepke,K. and Timmermann,B.
Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                          3451 bp
Sequence 6 from Patent W09937761
AX022522
                                                                                                                                                Patent: WO 9937761-A 6 29-JUL-1999;
                                                                                                                                                                    and use thereof
                                                                                                                                                                                                                                      unidentified
                                                                                                                                                                                                                                                  unidentified
                                                                                                                                                                                                                                                                               AX022522.1
                                                                                                                                                                                                                           unclassified
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15; Conserv
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Hoehe,M., Koepke,K. and Timmermann,B.
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                                                   /organism="unidentified"
/db_xref="taxon:32644"
873 c 897 g 89
                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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736 c 724 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 15; DB 6; 100.0%; Pred. No. 7.6e+02;
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Pred. No. 7.7e+02;
Pred. No. 7.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3451;
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l Similarity 100.0%;
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Sequence 4625 from Patent W00194629.
AX334116
                                                                                                                                                                                                    Avalon Pharmaceuticals (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
873 c 895 g 893
                                                                                                                                                                                      Location/Qualifiers
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/db_xref="taxon:9606"
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87092393
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Kobilka,B.K., Frielle,T., Dohlman,H.G., Bolanowski,M.A.,
Kobilka,B.K., Keller,P., Caron,M.G. and Lefkowitz,R.J.
Deli. ation of the intronless nature of the genes for the human and
hamster beta 2-adrenergic receptor and their putative promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for placelet-derived growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U., Caron,M.G. and Lefkowitz,R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobilka,B.K., Dixon,R.A., Frielle,T., Dohlman,H.G.
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M15169.1 GI:178201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adrenergic receptor.
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/GL_XTEE="GDB:GOO-120-541"
/CLTADS | GALDE:GOO-120-541"
/CLTADS | GALDE:GOO-120-541 | GALD
                                                                                                                                                                                                                                                  /product="beta-2 adrenergic receptor"
/protein_id="AAA88015.1"
/db_xref="GI:178202"
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/gene="ADRB2"
/note="b-2-adr mRNA (alt.); G00-120-541"
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/db_xref="GI:560761"
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1376. .3383
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/clone="pTF."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="ADRB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="b-2-adr mRNA (alt.); G00-120-541"
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1379. .3383
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/tissue_lib="Evan Sadler"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        id="AAA88014.1"
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Gragduate School of Pharmaceutical Sciences; 7-3-1 Hong
Bunkyo-ku, Tokyo 113-0033, Japan
(E-mail:ifujii@mol.f.u-tokyo.ac.jp, Tel:81-3-5841-4743,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces galilaeus (strain:3AR-33) DNA Streptomyces galilaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax:81-3-5841-4744)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujii, I. and Chung, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces 1 (bases 1 to 25883)
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                   /Translation="MITLYWDYLOEYENERADILDAVETVESSGRLVLGDSVRGEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                    ALVLGDNIFHGHHFYDLLQSNVRDVQGCVLFGYPVEDPERYGVGETDASGQLVSLEEK
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                                                                                                                                                           /product="Acl2"
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                                                                                                                                                                                                                                         /function="aminotransferase"
                                                                                                                                                                                                                                                                                                                                                 GYGRYVMAVAREFSG"
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                                                                                                                                                                                                                         /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Acly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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/function="dTDP-1-glucose synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(164. .1039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces
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Pred. No. 7.6e+02;
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Hongo,
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PPSMRFPVKQPFVPLRYIPYNGQAVIPDWLHEPPKKRRVCLTLGVAHREVLDGDRASI GELVKALAELDVEVVATLNGEAARRDGLPDNVRAVDEVPLNALLPTCSAVIHHGGSGT gene

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FGLDLLGRWRETFLDLQEERLPEQRDDPLREWLTWTLGRYGAEFEEEVAVGQWTVDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLDPEGFRAMYFPVGVGHAFIALEDDTVMSYMLSGSYEAQHEMSLSPLDPALGLPIPQ
DVAPILSARDTAAPLLEQVRAEGGLPEYDKCRRIEAALWRP"
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/function="glycosyltransferase"
                                                                                                                                                                                                                                                                                                                                                                               complement(5513. .6835)
                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="aclK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MQFRELAVSGAFVFTPPVFEDDRDLFTSPFQEPAFVAALGHPLF
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/gene="aclL"
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ESGGFFDVIGVSVTANGREVGGWRQAMIEPHGTGVIAFLMRRINGVEHVLVHARTEPG
YADVVELAPTVQCVPESYRWLPSAARPRHLDEVLAAGPDRIRFEAVLSEEGGRFFHAR
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                                                                                                                                                                                                                                                                                              /note-"putative"
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/transl_table=11
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KEFDGVPHFLMQAKAEPGNPGGLQLSPTVQATRSNYTGVHKGRPVPYLDYFRDTSRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="dTDP-hexose 2,3-dehydratase"
                                                                                                                                                                                                                                                                                                                                                                                                                                               5513.
                                                                                                                                                                                                                                                                                                                                                                                                                                            .6835)
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gene

CDS gene

100.0%;

0;

Pred. No. 6.7e+02; 0; Mismatches 0;

Indels

0; Gaps

0;

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ACM MIL
                                                                                                                                                                                   CDS
                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="ketoreductase"
/note="Registered with the DDBJ/EMBL/GenBank databases by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number is D14040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Translation="MAHEWITTEHTITVAAAPBAVEGLVERAODWPHVFDPSLHVEYL
ERSGEBERLRWATANGEVKSWTSRTILDRAGIRIGERGEVSODEVAAMGGEWIVEAL
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LLDBGEGDAWADIFTEDGTFDOSSTAEFVRGRAAIAAAVRGREPAAPAGTVRHWLGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8321, .9106)
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AAWRFPDGSVRTAYDALVVSTAAGAAPVIRLSTSCQDVLVADGDGWLVSHRYVGHDGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(6921 .8273)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6921. .8273)
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PSFAENCARIRREMYGTFSFNDIVPLLEKLTAEHRRDRGARGTVEGEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of akalli gene (12-JAN-1993). The accession
                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC103155
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                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
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TE 1 (Dases 1 to 54705)

RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burnell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Dathorne, S.R., David, R., David, R., Dardia, M.L., Davis, C., Chen, R., Dardy, Carrol, L., Ding, Y., Dinh, H.H., Douthwaits, V., Deigado, O., Dugan-Rocha, S., Dinh, H.H., Douthwaits, V., Deigado, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AC018327/c
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TITLE
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Matches 15; Conserve
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                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                         AC103155
                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                      AC103155.2 GI:17974642
                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-20114, *** SEQUENCING IN PROGRESS AC103155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was identified as CDM:10214360 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' Sequence.
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTCCGCCCGCTGAGG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12567 a
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42014 bp DNA linear HTG 09-DEC-1999

Fig. 1 PROGRESS ***, in ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
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| 8420 c 8766 g 12261 t
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100.0%;

Score 15; DB 2; ; Pred. No. 6.6e+02; Mismatches

Length 42014;

Gaps

0;

HTG 21-DEC-2001

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8766 g 12261 t

0,

CDS gene

CDS 9ene

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hollins, B., Homsi, F., Howard, S., Johnson, R., Jolivet, S., Jackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Johnson, R., Jolivet, S., Johnson, R., Jolivet, S., Johnson, R., Jolivet, R., Korvan, C., Karlsson, E., Kelly, S., Khan, G., King, L., Korvah, J., Joudah, S., Karlson, E., Kureshi, A., Landry, N., Leal, B., Lewis, L. Liu, W., Lio, L., Lio, R., Lio, R., Louier, R., Louier, R., Louier, R., Louier, R., Louise, G., Li, J., Li, J., Liu, W., Louise, R., Luna, R., Kovar, C., King, L., Luna, R., Kovar, C., King, L., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M., Meador, M., Meda, D., Metson, J., Newtson, N., Martinez, E., Massey, E., Mawhiney, E., McLeod, M., Metson, N., Worgan, M., Noris, S., Noser, M., Neda, D., Newtson, J., Newtson, N., Morgan, M., Noylen, M., Nickerson, E., Newkenkwo, S., Wei, G., Metzker, M., Nolas, R., Pace, A., Payton, B., Noylen, M., Payton, B., Polies, M., Rojas, A., Rojubokan, I., Shooshtari, N., Opiesy, M., Rojas, A., Rojubokan, I., Shooshtari, N., Sisson, I., Sodergren, B., Scherer, S., Scatt, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, B., Svatek, A., Tabor, P., Tamerisa, A., Thomas, N., Stone, H., Sutton, A., Taylor, T., Yera, M., Stanley, H., Tansey, J., Wasquez, J., Vera, V., Washington, C., Taylor, V., Vera, V., Washington, C., Walliamson, A., Washington, C., Walliamson, A., Washington, C., Walliamson, A., Washington, C., Walliamson, A., Wu, Y., Zorrilla, S., Nelson, D., Vinson, R., Weinstock, G., and Gibbs, R.
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Estaj,C., Escotto,M., Gabisi,A., Gao,J., Garcia,A., Garner, Hale,S.,
Foster,P., Frantz,P., Gorrell,J.H., Guevard,W., Gunarathe,P., Hale,S.,
Garza,N., Gill,R., Gorrell,J.H., Harth,M., Havlak,P., Hawes,A.,
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Hernandez,J., Harris,C., Hodyson,A., Hogues,M., Holloway,C.,
Hernandez,J., Hodyson,A., Hodyson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genome Sequence Version replaced gi:17062799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft.draft
                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 42106 bases at least Q40 consensus quality: 46901 bases at least Q30 consensus quality: 50808 bases at least Q20 consensus quality: 50808 bases at least Q20 consensus quality: 50808 bases at least Q20 estimation consensus quality: 23322; sum-of-contigs estimation guality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 0.2x in Q20 bases; sum-of-contigs estimation quality coverage: 0.2x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: CJIW
Center clone name: CH230-20114
Center Summary Statistics
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20867: contig of 1334
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24587: contig of 1582 bp in length
24687: gap of unknown length
26166: contig of 1479 bp in length
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Estimated Total Number of Errors is 0.1.
Location/Qualifiers
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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## ALIGNMENTS

(first entry)

Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5931(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; WPI; 2000-400107/34. Liggett SB; (UYCI-) UNIV CINCINNATI. 25-NOV-1998; 24-NOV-1999; 02-JUN-2000 WO200031307-A1 Homo sapiens allele-specific oligonucleotide primer; ss Human beta2 adrenergic receptor beta2AR C allele-specific primer #2. 98US-0109886 99WO-US27963.

Claim 1; Page 162; 484pp; English.

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AAH79739/c
ID AAH797
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                       Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
               diseases and infections
                                                                                                                                            Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoglycerate kinase; immunosuppressive; immunostimulatory;
antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     major histocompatibility complex Class I histocompatibility antigen; MHC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-hydroxybutyrate; dehydrogenase; protein therapy; adenosine triphosphate-dependent RNA helicase;
                                                                                                                                                                                                                     27-DEC-1999;
                                                                                                                                                                                                                                                                                             05-JUL-2001
                                                                                                                                                                                                                                                                                                                                  WO200148245-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA containing single nucleotide polymorphism SEQ ID NO.
                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                        27-DEC-2000; 2000WO-US35346
                                                                                                                                                                                                                                                                                                                                                                                                            antileukemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; single nucleotide polymorphism; SNP; angiopoletin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH79739;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which regulates expression of the beta2NR gene. The polymorphism is thought to affect individuals, responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity dishates regular disease, ischemic heart disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5 leader sequence, which encodes a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 1 A; 6 C; 11 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              individual to these diseases and determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 12; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCCTGGGGGGGGCGCCTCAGCGG 20
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                                                                                                     2001-418297/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is an allele-specific oligonucleotide primer the C allele of the human beta2 adrenergic receptor (beta2AR) gene,
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                                                                                                                                          Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; antimicrobial; gene therapy; vaccine; ds.
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                                                                                  antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic, antirheumatic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to angiopoietin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) class I histocompatibility antigen and/or phosphoglygerate kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia) diseases of the nervous system, an infection of pathogenic organisms. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to angiopoietin, 4-hydroxybutyreins (dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) class I histocompatibility antigen and/or phosphoglycerate kinase. These nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
                                      be used to alter phenotypic traits such as longevity, appearance, strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins have potential immunosuppressive, immunostimulatory,
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Matches Query Match Best Local : 44 Local Similarity 1 GGCTGGGGGCGCCTCAGCGG 20 GECTGGEGGCGCCTCAGCGG 20; Conservative 100.0%; 100.0%; 0; Score 20; Pred. No. 10; Mismatches DB 22; 0; Length 51; Indels 0; Gaps

0;

Sequence 51 BP; 5 A;

24 C; 18 G; 4 T; 0 other;

D,

AAH27139/c RESULT 3 Human beta-2 adrenergic receptor UTR region with RBP binding ability. 08-AUG-2001 AAH27139; AAH27139 standard; DNA; 230 BP (first entry)

stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration;

Homo sapiens.

WO200134624-A1

17-MAY-2001

09-NOV-2000; 2000WO-US30888

10-NOV-1999; 9905-0437458

(MESS-) MESSAGE PHARM INC

Giordano A, Xavier AK;

WPI; 2001-335904/35.

neurodegeneration New nucleic acids that bind RNA-binding proteins or regulate mRNA function, useful for therapeutic gene regulation, such as in cases of

Claim 1; Page 28; 33pp; English.

Sequences AAH27132 - AAH27151 represent human gene untranslated regions

Qγ g

AAA38784 standard; DNA; 2340 BP

Best Local Similarity

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Conservative

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Score 20; DB Pred. No. 9.5; Mismatches

DB 18; Length 1999;

Query Match

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Best Local :
                                   This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used is screening for agonists and antagonists, which are useful in researching
                                                                                                                       Disclosure; Page 27-30; 47pp; Japanese.
                                                                                                                                                     agonists and antagonists and researching asthmatic diseases
                                                                                                                                                                    Novel beta-2 adrenalin receptor sub-type - useful for screening for
                                                                                                                                                                                                                                                                 Fujii K,
                                                                                                                                                                                                                                                                                            (DAIN ) DAINIPPON PHARM CO LTD
                                                                                                                                                                                                               P-PSDB; AAW34320
                                                                                                                                                                                                                                                                                                                              27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                               24-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                              W09735963-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthmatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-2 adrenalin receptor subtype coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT93250 standard; cDNA to mRNA; 1999 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for therapeutic regulation of gene expression, such as in cases of neurodegeneration; stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorders (obesity and diabetes) and bacterial or viral infection. The present sequence is one of gene fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBPs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP interaction or mRNA functionality; or RBPs that interact with the compounds. Compounds identified using the gene fragments are potentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity. RBPs mediate the processing of pre-mRNA, the transport of mRNA from the nucleus to the cytoplasm, mRNA stabilisation, translational efficiency, and the sequestration of some mRNAs. Therefore modification of post-transcriptional protein expression in eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention, isolated from the human beta-2 adrenergic receptor gene.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                          Nomura A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                          Yano K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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AAA38784/c
XX
XX
AC AAA3871
XX
DT O5-OCT
XX
Human;
KW Human;
KW Chromos
XW Cohromo
XW Cohromo
XW Cohromo
XW Cohromo
XW Cohromo
FT Chos
FT Chos
FT Sig_p
FT allel
FT allel
FT allel
FT allel
FT W0200
XX
XX
PT W0200
XX
YX
YX
YX
PT W0200
XX
YX
PT Ligg
XX
YX
PT Poly
PT Poly
PT Gos
PT Foce
PT Gise
PT Gos
XX
XX
Disc
XX
CC The
CC The
CC Seq
CC inf
CC Con
         The present sequence is a fragment of the C allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5931 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension,
congestive heart failure, ischemic heart disease, arrhythmia, obesity
                                                                                                                                                                                                                                           Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                            Disclosure; Figure 1; 56pp; English.
                                                                                                                                                                                                                                    hypertension
                                                                                                                                                                                                                                                                                                                                                         Liggett SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                      WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                                                                            (UYCI-) UNIV CINCINNATI.
                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200031307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human beta2 adrenergic receptor beta2AR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anaphylaxis; chronic obstructive pulmonary disease; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA38784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           980S-0109886
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US27963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
1588...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(1541,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= 5'_leader_cistron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1487..1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /partia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "no stop codon given at 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*lag= a
/product= "beta2 adrenergic receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1487..2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end of sequence"
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Sequence 1999 BP; 477 A;

513

0

485

G;

524 T; 0 other

The protein can be used in

asthmatic diseases.

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AAV52614/c
ID AAV526
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8888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                      This cDNA sequence codes for human beta-2-adrenergic receptor (see AAW75777) having an arginine residue at position 16. A novel metho for identifying individuals susceptible to adverse responses to regular administration of beta-agonists comprises: (a) identifying in a genomic nucleic acid sample from the individual first and second alleles of the beta 2-adrenergic receptor gene, and (b) classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor gene alleles may be
                                                                                                                                                                                                             Diagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patient homozygous for allele encoding Arg at position 16 of beta2-adrenergic receptor protein
                                                                                                                                                                                  Disclosure; Page 33-35; 46pp; English.
                                                                                                                                                                                                                                                                                             WPI; 1998-506372/43.
                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV52614 standard; cDNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1559 GGCTGGGGGGCGCCTCAGCGG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be seen the susceptibility of an individual to these diseases and
identified by any known method e.g. denaturing gel electrophoresis or PCP amplification (see also AAV52615-17). Identification
                                                                                                                                                                                                                                                                                                                                         MdILIB
                                                                                                                                                                                                                                                                                                                                                       Boushey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09839477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-2-adrenergic receptor; human; asthma; beta-agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta-2-adrenergic receptor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV52614;
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                                                                                                                                                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGCTGGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 100.0%; Score 20;
Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the best treatment.
                                                                                                                                                                                                                                                                                                                                                       Chinchilli VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0811441
                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US03908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "A to G substitution, results in Argl6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to Gly amino acid change"
                                                                                                                                                                                                                                                                                                                                                      Drazen JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                    Fish JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 2340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                            patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1559 GGCTGGGGGCGCCTCAGCGG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known polymorphism in the beta 2-adrenergic receptor gene as being linked
                                                                                                                          30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke; neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                          30-DEC-1998;
                                                                                                                                                                                      29-JUL-1999
                                                                                                                                                                                                                        W09937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         post-traumatic stress disorder; autonomous nervous system disease;
metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta 2-adrenergic receptor DNA variant 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ00776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ00776 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and individuals homozygous for Arg16 are more susceptible.
                                                                                          (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCTGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                          Koepke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                          97DE-1058401.
                                                                                                                                                          98WO-DE03818.
                                                                                                                                                                                                                                                                   /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Glu
                                                                                                                                                                                                                                                                                                                                                                                            /note= "This nucleotide differs from the wild type
    nucleic acid sequence represented in AAZ00773
    and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                    replace(1666,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1633,a)
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                          Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                           wild type amino acid sequence from an Gly
                                                                                                                                                                                                                                                      residue to Gln residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Human beta2-adrenergic receptor gene variants, useful for

WPI; 1999-479048/40.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                           mutation
                                                                                                                                                                      mutation
                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective nordernergic-receptor
                                                                                                                                                                                                                                                                                                                                                                         metabolic
                                                                                                                                                                                                                                                                                                                                                                                neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; motablic illestress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                      neuropsychiatric disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta 2-adrenergic receptor DNA variant 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA200779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ00779 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1559 GGCTGGGGGGCGCCTCAGCGG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 2a; 27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGCTGGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                     illness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                   /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                  replace(1633,a)
                                                                                                                                                                                                                                      Location/Qualifiers
replace(1568,t)
/note= "This nucleotide differs from the wild type
                    /*tag=
                                       replace(1666,c)
                                                                                                                                                                                                  /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                               gene therapy; pharmaceutical intervention therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                       wild type amino acid sequence from an Gly
                                                                                                                                                                               nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 2
Pred. No. 9.4;
                                                        to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
 RESULT 9
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В
                                                                                                                                                          PXX FTT
                                                                             Matches
                                                                                                                Query Match
                                                                                                                                                                                       determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke, other conditions that can be
1559 GGCTGGGGGCGCCTCAGCGG 1540
                                                                                                                                                                                                                                                                                                   and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be
                                                                                                                                                                                                                                                                                                                                                                                                                     determined include neuropsychiatric disease, such as depression, anxiattention deficit disorder with hyperactivity, eating disorders, e.g.
                                                                                                                                                  Sequence 3451 BP; 789 A; 873 C; 897 G; 892 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                   anorexia nervosa and bulimia, or post-traumatic stress disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               determining an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1999
                                                                                             тосат
                                      1 GGCTGGGGGGGCCTCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                   the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                                                                             20;
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koepke K,
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DE-1058401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Timmermann
                                                                                           100.0%;
                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wild type amino acid sequence from an Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue to Gln residue"
                                    20
                                                                         0;
                                                                                           Pred.
                                                                                                              Score 20;
                                                                       Mismatches
                                                                                             N
O
                                                                                       9.4;
                                                                                                          DB 20; Length 3451;
                                                                         0;
                                                                         Indels
                                                                         0
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                            anxiety,
                                                                     0;
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post-traumatic stress disorder; autonomous nervous system disease; metabolic illness; gene therapy; pharmaceutical intervention thera

eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;

hyperactivity;

neuropsychiatric disease; attention deficit disorder;

neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;

Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;

Human beta 2-adrenergic receptor wild type DNA.

07-OCT-1999 AAZ00773;

(first entry)

AAZ00773 standard; DNA; 3451

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THE THE PROPERTY OF THE PROPER
 AA200774" mutation
                                                                                                                                                        mutation
                                                                           AA200774"
                                                                                                                                                                                                                                                   AAZ00774" mutation
                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                           mutation
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                                     /note=
                                                                                                                                      replace(2110,a)
/*tag= m
                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(1666,g)
/*tag= j
                                                                                                                 /note=
                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                             replace(1839,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(1633,g)
/*tag= i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(159,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                "This mutation results in a change in the corresponding wild type amino acid sequence from a Thr residue to Ile residue"
                                                                                                                                                                                                                                                                                                                                                                              "This mutation results in a change in the corresponding wild type amino acid sequence from a Gln residue to Glu residue in the
                                                                                         "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                             "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This mutation results in a change in the
                                 "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "This mutation results in a change in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "This nucleotide differs from the wild type sequence in the sequence represented in
sequence in the sequence represented in replace(2826,a)
                                                                                                                                                                                                                                                                                                                                             variant sequences represented in AA200774,
AAZ00776, AAZ00779"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from an Arg residue to Cys residue in the variant sequences represented in AAZ00774, AAZ00775, AAZ00777, AAZ00778 and AAZ00780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding wild type amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ00776, AAZ00777, AAZ00779 and AAZ00780'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variant sequences represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponding wild type amino acid sequence from an Arg residue to Gly residue in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the variant nucleotide sequences represented
in AAZ00774 and AAZ00779"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence in the sequence represented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence in the sequence represented in
                                                                         replace(2640,c)
                                                                                                                                                                                                                                                 replace(2078,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace(1221,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1120,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(934,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(565,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(245,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ00774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                 RESULT 10
AAA38339/c
Вb
                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                             Beta-adrenergic receptor-2 gene; regulatory region; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                           1559 GGCTGGGGGCGCCTCAGCGG 1540
           Homo sapiens
                                                 stroke; prognosis; drug screening; treatment outcome; human; ds
                                                                                                                                            Human beta-adrenergic receptor-2 gene regulatory region
                                                                                                                                                                                                                          AAA38339;
                                                                                                                                                                                                                                                             AAA38339 standard; DNA; 3451 BP
                                                                                                                                                                                    21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                              1 GGCTGGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                    (first entry)
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Mismatches

0;

Indeis

0;

Gaps

0;

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or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents the wild type human beta 2-adrenergic receptor gene which is described in the method of the invention.
                                                                                                                                                                   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervosa and bulimia, or post-traumatic stress disorder. Diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPT; 1999-479048/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koepke K, Timmermann B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97DE-1058401
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                                        100.0%; Score 20; DB; 100.0%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
0;
                                                                             DB 20;
                                                                        Length 3451;
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Matches
                                                                                                                                           Best Local Similarity
1559 GGCTGGGGGCGCCTCAGCGG 1540
                                                                                                                                                                                                                                                                                                     sequence represents the human beta-adrenergic receptor-2 ge or regulatory region (GenBank M15169, J02728, M16106). The polymorphic sites identified are 934A/G, 987C/G, 1006A/G, 1120C/G, 1221C/T,
                                                                                                                                                                                                                                                                                                                                                                                     exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which turn decreases the duration and cost of such trials. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eliminates trial and error in selecting a treatment for a particula individual cardiovascular patient. It also provides the ability to eliminate patients from clinical trials who are predicted to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen. Fragments of the genes comprising a polymorphic site may be used as
                                                                                                                                                                                                                        Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular disorders such as myocardial infarction, unstable angina hypertension, atherosclerosis and stroke. They are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             status in an individual and to newly identified polymorphisms in t genes encoding angiotensin converting enzyme (ACE), angiotensin II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or more polymorphic positions within these genes, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 123-124; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptors 1 and 2. The method comprises determining the sequence at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding specific proteins, with reference polymorphic pattern
                                                                                                                                                                                                                                                                                      '541C/T and 1568C/T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norberg LT, Andersson MK, Lindstrom PHR, Jonsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200022166-A2
                                                     1 GGCTGGGGGGCGCCTCAGCGG 20
                                                                                                                20;
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0104286
98US-0104302
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                                                                                                                                  100.0%; Score 20; DB 2
100.0%; Pred. No. 9.4;
                                                                                                             0;
                                                                                                                Mismatches
                                                                                                                                                               DB 21;
                                                                                                          0;
                                                                                                                                                               Length 3451;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for a particular
                                                                                                          0;
                                                                                                    Gaps
                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                        FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XW XXX XXX XXX
                                               13-APR-2000; 2000WO-US10125
                                                                                                 13-APR-2000;
                                                                                                                                                                                                                  WO200179252-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; beta2-adrenergic receptor; beta2AR polymorphism; asthma; chromosome 5q31-32; migraine; congestive heart failure; hypertension; ischaemic heart disease; chronic obstructive pulmonary disease; COPD; obesity; diabetes mellitus; premature labour; vasotropic; cardiant; antiarrhythmic; antiasthmatic; antidiabetic; tocolytic; ds.
                                                                                                                                                            25-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS18444 standard; DNA; 3451 BP
                                                                                                    2000WO-US10125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                            replace (2110, A)
                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Polymorphic site 6 (PS6)"
replace (1541, T)
                                                                                                                                                                                                                                                                                                                                                       /note= "Polymorphic site 12 (PS12)"
                                                                                                                                                                                                                                                                                                                                                                                                                  replace (2078,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Polymorphic site 7 (PS7)"
replace (1568, C)
                                                                                                                                                                                                                                                                 /note= "Polymorphic site 13 (PS13)"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Polymorphic site 11 (PS11)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Polymorphic site 9 (PS9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Beta2AR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1588..2829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace (1221,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Polymorphic site 5 (PS5)"
replace (1221, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Polymorphic site 4 (PS4)"
replace (1182, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Polymorphic site 8 (PS8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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"Polymorphic site 1 (PS1)" e (879, A)

(565, A)

(1120,

site 3 (PS3) "

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Stack CB,
Liggett SB;
                                             (UYCI-) UNIV CINCINNATI
                                                             (GENA-) GENAISSANCE PHARM INC
              Drysdale CM, Stephens JC,
              Nandabalan K,
              Judson RS
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"Polymorphic site 10 (PS10)"

(1839, A)

(1666, G)

(1633, G)

В

AAS18444/c RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for therapeutic purposes such as treating disorders affected by expression or function of beta2AR such as congestive heart failure, arrhythmia, ischaemic heart disease, hypertension, migraine, asthma, chronic obstructive pulmonary disease (COPD), obesity, diabetes and premature labour. The method is useful for determining the frequency of a beta2AR genotype or haplotype in a population. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to polymorphisms and haplotypes of the human beta2-adrenergic receptor (beta2-AR) gene located on chromosome 5q31-32, and methods for haplotyping and/or genotyping the beta2AR gene in an individual. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers for detecting the beta2AR gene polymorphisms. The beta2AR gene polymorphisms are useful in studying the expression and biological function of beta2AR, and for developing drugs targeting this receptor. They are also useful for the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 5q31(12); disease predisposition; asthma; hyperten congestive heart failure; ischemic heart disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1559 GGCTGGGGGCGCCTCAGCGG 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated beta 2-adrenergic receptor polynucleotide, useful for studying expression and biological function of receptor and for developing drugs targeting receptor, comprises polymorphism of adenosine at PS2 and thymine at PS5 -
                                                      WPI; 2000-400107/34.
                                                                                                                                                                          (UYCI-) UNIV CINCINNATI
                                                                                                                                                                                                                                           25-NOV-1998;
                                                                                                                                                                                                                                                                                                     24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200031307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allele-specific oligonucleotide primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human beta2 adrenergic receptor beta2AR T allele-specific primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA46130 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the polymorphisms in the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a reference sequence for the human beta2AR gene which shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAU10763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGCTGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetes; vascular disease; premature labour; migraine;
xis; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                        98US-0109886
                                                                                                                                                                                                                                                                                                     99WO-US27963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB :
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD) The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and determine the best treatment.
                                                                                                                                  beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour,
                                                                                                                                                                                                                  which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and
Sequence 20 BP; 2 A; 6 C; 10 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 12; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an allele-specific oligonucleotide primer for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypertension -
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Matches 1 GGCTGGGGGGCGCCTCAGCAG 1 GGCTGGGGGCGCCTCAGCGG 20 Similarity Conservative 92.0%; 95.0%; 20 0: Score 18.4; Pred. No. 52 Mismatches DB 21; Length 20; Indels 0; Gaps 0,

Вþ

AAX61116/c RESULT 13 AlphalB-adrenergic receptor; human; cardiovascular disease; beta2 adrenergic receptor; genetic variation identification; hypertrophy; disease diagnosis; hypertrension; prostatic disease; pulmonary disorder; asthma; peripheral vascular disorder; neuropsychic disorder; AAX61116 standard; DNA; 2300 BP endocrine-metabolic disorder; ss. Human beta2-adrenergic receptor gene. 27-JUL-1999 (first entry)

Homo sapiens

W09924454-A1

20-MAY-1999

04-NOV-1998; 98WO-US23496

10-NOV-1997; 97us-0086232

(REGC ) UNIV CALIFORNIA

Buescher R, Herrmann V, Insel PA;

WPI; 1999-327357/27.

Pairs of oligonucleotides for amplifying adrenergic receptor genes

Disclosure; Fig 2; 58pp; English.

This sequence represents the human beta2-adrenergic receptor gene, and is amplified by the primers of the invention. The primers are non-self hybridising; contain at least 15 nucleotides (nt) and has a melting temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising; anneals to two distinct segments (separated by at least 400 nt); and

Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic

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RESULT 14
AAA38340/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic
                                                                      status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (ATI) and type 2 (ATI2), angiotensinogen (AGT), renin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostatic disease (hypertrophy), and those in the beta2 gene with cardiovascular disease, hypertension and asthma, but variations may also be associated with peripheral vascular, pulmonary, neuropsychic and endocrine-metabolic disorders. These primers allow rapid and specific amplification of large and homogeneous gene segments of the alphalB and beta2 genes from a complex mixture of DNAs. This makes possible detection
                                  aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one
                                                                                                                                                                          Disclosure; Page 124-125; 126pp; English.
                                                                                                                                                                                                                                 Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-adrenergic receptor-2 gene; coding region; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; ath
                                                                                                                                     The invention relates to a novel method of assessing the cardiovascular
                                                                                                                                                                                                                encoding specific proteins, with reference
                                                                                                                                                                                                                                                                                             WPI; 2000-318010/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200022166-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stroke; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta-adrenergic receptor-2 coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA38340 standard; DNA; 2305 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        (EURO-) EURONA MEDICAL AB
                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variations for diagnosis of disease. Specifically variations in the alphalB gene are associated with cardiovascular disease, hypertensic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence complementary to a template sequence in a DNA polymerase reaction. The primers are used to amplify segments of the alphalB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   generates a homogeneous population of gene segments in a polymerase chain reaction (PCR). At least one primer in the pair can extend a 3'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    large-scale sequencing analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta2 adrenergic receptor genes, particularly to identify genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            765 GGCTGGGGGGCGCCTCAGCAG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGCTGGGGGCGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic alterations not previously amenable to routine, automated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                  Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                                               98US-0104302
                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0104286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB01678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug screening; treatment outcome; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%;
                                                                                                                                                                                                                                                                                                                                  Lindstrom PHR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                              polymorphic pattern
                                                                                                                                                                                                                                                                                                                                  Jonsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 15
AAZ00774/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  뮰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which in
                                                                                                                                                                                                                                                                                                                                                        eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ00774 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        turn decreases the duration and cost of such trials. The present sequence represents the human beta-adreneryic receptor-2 gene coding region (GenBank Y00106/g293708). The polymorphic sites identified are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a
                                                                                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta 2-adrenergic receptor DNA variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ00774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to
                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    metabolic illness; gene therapy; pharmaceutical intervention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment regimen comprising administration of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2068 no insert/G/C and 2070 no insert/C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 individual cardiovascular patient. It also provides the ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           765 GGCTGGGGGGCGCCTCAGCAG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (e.g., ACE inhibitors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGCTGGGGGGGGCCTCAGCGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                replace(159,t)
                                                                                         /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18.4;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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mutation

replace(245,a)

/\*taq=

/note= "This nucleotide differs from the wild type

nucleic acid sequence

represented in AA200773"

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IN THE REPORT OF THE PROPERTY 
                    30-DEC-1997;
                                                                              30-DEC-1998;
                                                                                                                                     29-JUL-1999
                                                                                                                                                                                         W09937761-A1
                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation
                                                                           98WO-DE03818
                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                            replace(2826,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This nuclectide differs from the wild type
nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                              /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(2640,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(2078,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(1541,t)
/*tag== g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace(1839,g)
/*tag===k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replace(1666,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(1568,t)
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(1221,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(1120,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replace(934,g)
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(565,g)
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Cys residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AA200773 and results in a Change in the corresponding wild type amino acid sequence from an Ile residue to Thr residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Gluresidue to Gln residue"
                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wild type amino acid sequence from an Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid sequence represented in AAZ00773"
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individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                            disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individual specific beta
                                                                                                                                                                                                                                                             attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Eggleston, sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be
                                                                                                                                                                                                                                                                                                                                                               determined include neuropsychiatric disease, such as depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-479048/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                 including
                                                                                                                                                                                                                                                                                                                                                               anxiety,
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Search completed: November Job time: 84.7273 secs 2, 2002, 16:13:18

Дb QΥ

1559 GGCTGGGGGGCGCCTCAGCAG 1540

1 GGCTGGGGGCGCCTCAGCGG 20

Matches Query Match Best Local

19; Similarity

Conservative

0;

92.0%; 95.0%;

Score 18.4; Pred. No. 45; Mismatches

DB 20; Length 3451; Indels

0,

Gaps

0;

Local

Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;

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November 2, 2002, 13:09:44 ; Search time 82.7273 Seconds (without alignments) 415.078 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*/SIDS1/gcgdata/geneseq/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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                                Compugen Ltd.
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                     1 cccgccgtgggtccgcccg 20
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDSI/gcgdata/geneseg/genesegn-embl/NA1998.DAT:\*
/SIDSI/gcgdata/geneseg/genesegn-embl/NA1999.DAT:\*
/SIDSI/gcgdata/geneseg/genesegn-embl/NA2001.DAT:\*
/SIDSI/gcgdata/geneseg/genesegn-embl/NA2011.DAT:\*
/SIDSI/gcgdata/geneseg/genesegn-embl/NA20018.DAT:\*
/SIDSI/gcgdata/geneseg/genesegn-embl/NA20018.DAT:\*

	Description	Human beta2 adrene	Human DNA containi	Himan beta-2 adren	Beta-2 adrenalin r	Himan hetal adrene	Human beta-2-adren	Human beta 2-adren	Human beta 2-adren	Human beta 2-adren
SUMMARIES	QI	AAA38788	AAH79739	AAH27139	AAT93250	AAA38784	AAV52614	AA200776	AA200779	AAZ00773
	DB	21	22	22	38	21	19	20	20	20
	Match Length DB I	20	51	230	1999	2340	3451	3451	3451	3451
ope (	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	20	20	20	20	20	20	20	20	20
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Human beta-adrener	Reference sequence	Human beta2 adrene	Human beta2 adrene	1	beta-	beta	heta 2	heta 2	beta 2	heta 2	2 adren	Perilla flavone sv		Drosophila melanog	Human secreted pro	Human KCC4 genomic						strain	treptomyces	HSV-2 strain SB5 C	ohila me	HSV-2 strain SB5 C	Human herpesvirus	The rat beta-actin	N. meningitidis pa	Neisseria meningit	N. meningitidis B	Template switching		Switchi	~
AAA3833	AAST844	AAA4612	AAA3878	AAX6111	AAA38340	-	AA200775	AA200777		AAZ00780						AAS59448				AAS29788				AAV62154								AAT9847		AAT9849	AAZ28717
21	7.4	21	7.1	20	21	20	20	20	20	20	18	22	23	23	21	22	22	21	21	22	22	13	22	13	23	19	24	16	21	21	21	18	18	18	20
3451	245T	20		2300	2305	3451	3451	3451	3451	3451	1400	1770	675	8100	292	320	624	739	882	1052	10934	12488	14806	21034	73947	117213	154746	4100	65632	49	1437668	40	40	40	40
100.0	T00.0	92.0	0.26	92.0	92.0	95.0	95.0	92.0	92.0	92.0	84.0	82.0	80.0	80.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	79.0	77.0	77.0	77.0	77.0	76.0	76.0	76.0	76.0
20	٧,	187	o.	ω.	18.4	18.4	18.4	18.4	18.4	18.4	vo-	9	16	16	15.8	15.8	15.8	5	'n.	'n.		15.8		'n		'n		S)		S.	S.		15.2		
10	<b>⊣</b> .	77.	ς ·	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
												O	O	O	O	O	U	υ	O		U		O	U		O	O		U			υ	υ	υ	O

## ALIGNMENTS

RESULT 1

Human beta2 adrenergic receptor beta2AR C allele-specific primer #1. chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; allele-specific oligonucleotide primer; ss. Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; AAA38788 standard; DNA; 20 BP 05-OCT-2000 (first entry) AAA38788; AAA38788 

Homo sapiens.

WO200031307-A1. 02-JUN-2000

99WO-US27963. 24-NOV-1999; 98US-0109886. 25-NOV-1998;

(UYCI-) UNIV CINCINNATI.

Liggett SB;

WPI; 2000-400107/34.

Claim 1; Page 162; 484pp; English.

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RESULT 2
AAH79739
ID AAH7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which is located on chromosome 5931 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the Tallele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary diseases (COPD). The gene can, therefore, be used to predict the susceptibility of an
               diseases and infections
                             Polymorphic nucleic acids encoding e.g. angiopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                         phosphoglycerate kinase; immunosuppressive; immunostimulatory;
antirheumatic; antisclerotic; antidiabetic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4-hydroxybutyrate; dehydrogenase; protein therapy;
adenosine triphosphate-dependent RNA helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                         WPI; 2001-418297/44
                                                                                                                                                Shimkets RA,
                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                       27-DEC-1999;
                                                                                                                                                                                                                                                            27-DEC-2000; 2000WO-US35346
                                                                                                                                                                                                                                                                                                 05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              major histocompatibility complex Class I histocompatibility antigen; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; single nucleotide polymorphism; SNP; angiopoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA containing single nucleotide polymorphism SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH79739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH79739 standard; DNA; 51 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an allele-specific oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the C allele of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 11; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an, therefore, be used to predict the susceptibility of an to these diseases and determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 0 A; 11 C; 7 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                              Leach M:
                                                                                                                                                                                                                       99US-0472688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human beta2 adrenergic receptor (beta2AR) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB
100.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to angiopoletin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phosphoglycerate kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia,) diseases of the nervous system, an infection of pathogenic organisms. They may also
                                                      strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                          proteins have potential immunosuppressive, immunostimulatory, antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostati antileukemic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class I histocompatibility antigen and/or phosphoglycerate kinase. These nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acids (AAH79386-AAH80036) encoding polymorphic variants of proteins (AAG98010-AAG98238) related to angiopoletin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
                                                                         be used to alter phenotypic traits such as longevity, appearance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ATP)-dependent RNA helicase, major histocompatibility complex (MHC
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Best Loc
Matches
                                                       Query Match
                                              Local
                 1 CCCCGCCGTGGGTCCGCCCG 20
8 CCCCGCCGTGGGTCCGCCCG 27
                                              Similarity
                                     Conservative
                                            100.0%;
                                                       100.0%;
                                     0;
                                              Pred. No.
                                                      Score 20;
                                     Mismatches
                                   0
                                                     Length 51;
                                    Indels
                                   0;
                                   Gaps
                                   0;
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Sequence 51 BP; 5 A; 24 C; 18 G; 4 T; 0 other;

g Qy

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RESULT 3
AAH27139
Human beta-2 adrenergic receptor UTR region with RBP binding ability.
                                               08-AUG-2001 (first entry)
                                                                                               AAH27139;
                                                                                                                                     AAH27139 standard; DNA; 230 BP
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Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration; stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.

WO200134624-A1

17-MAY-2001

09-NOV-2000; 2000WO-US30888

10-NOV-1999; 99US-0437458

(MESS-) MESSAGE PHARM INC

Giordano A, Xavier AK;

WPI; 2001-335904/35.

New nucleic acids that bind RNA-binding proteins or regulate mRNA function, useful for therapeutic gene regulation, such as

of.

Claim 1; Page 28; 33pp; English.

Sequences AAH27132 - AAH27151 represent human gene untranslated regions

0;

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ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                  This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used in screening for agonists and antagonists, which are useful in researching
                                                                                                                   Disclosure; Page 27-30; 47pp; Japanese.
                                                                                                                                                   agonists and antagonists and researching asthmatic diseases
                                                                                                                                                              Novel beta-2 adrenalin receptor sub-type - useful for screening for
                                                                                                                                                                                                                                                                                                                 27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-2 adrenalin subtype; cyanopindrol; agonist; antagonist; asthmatic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-2 adrenalin receptor subtype coding sequence.
                                                                                                                                                                                                                                                                                (DAIN ) DAINIPPON PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                 24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                               WO9735963-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT93250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT93250 standard; cDNA to mRNA; 1999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for therapeutic regulation of gene expression, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBPs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity. RBPs mediate the processing of pre-mRNA, the transport of mRNA from the nucleus to the cytoplasm, mRNA stabilisation, translational efficiency, and the sequestration of some mRNAs. Therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation; metabolic disorders (obesity and diabetes) and bacterial or viral infection. The present sequence is one of gene fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention, isolated from the human beta-2 adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegeneration; stroke; cardiovascular disease; hypertension; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interaction or mRNA functionality; or RBPs that interact with the compounds. Compounds identified using the gene fragments are potentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 CCCCGCCGTGCGTCCGCCCG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-489627/45.
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                                                                                                                                                                                                                                                 Furutani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                              96JP-0072914.
                                                                                                                                                                                                                                                                                                                                               97WO-JP00982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                               Kawashima H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                               Nomura A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T; 0 other

congestive heart failure, ischemic heart disease, arrhythmia, obesity,

asthmatic

diseases

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RESULT 5
AAA3807A 4
ID APA64
ID APA64
ID APA64
AID APA64
AID APA63
AX APA64
AX HUMA
XX HUMA
KW CONG,
K
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Best Local Similarity
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           The present sequence is a fragment of the C allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension,
                                                                                                                                                                                                                                                                                                                                                                               Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; adrenergic receptor; beta2ar; chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; ds.
                                                                                                                                                                                                                                                                                                     Disclosure; Figure 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                             hypertension -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-400107/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liggett SB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta2 adrenergic receptor beta2AR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA38784;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 CCCCGCCGTGGGTCCGCCCG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "beta2 adrenergic receptor"
/note= "no stop codon given at 3' end of sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 1487..2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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This cDNA sequence codes for human beta-2-adrenergic receptor (see AAW75777) having an arginine residue at position 16. A novel methofor identifying individuals susceptible to adverse responses to regular administration of beta-agonists comprises: (a) identifying in a genomic nucleic acid sample from the individual first and second alleles of the beta 2-adrenergic receptor gene, and (b) classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor gene alleles may be identified by any known method e.g. denaturing gel electrophoresis or PCR amplification (see also AAV52615-17). Identification
                                                                                                                                                                                 Disclosure; Page 33-35; 46pp; English.
                                                                                                                                                                                                          Diagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patient homozygous for allele encoding Arg at position 16 of beta2-adrenergic receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-1997;
                                                                                                                                                                                                                                                                                       P-PSDB; AAW75777
                                                                                                                                                                                                                                                                                                                                             Boushey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09839477-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-2-adrenergic receptor; human; asthma; beta-agonist; polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human beta-2-adrenergic receptor cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determine the best treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCCGCCGTGGGTCCGCCCG 20
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                                                                                                                                                                                                                                                                                                                                             Chinchilli VM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "A to G substitution, results in A-716 to Gly amino acid change"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           Drazen JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        Fish JE,
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                                                                                                                                                                                                                                                                                                                                          Ford
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                                                                                                                                     A novel method
                                                                                                                                                                                                                                       patients
                                                                                                                                                                                                                                                                                                                                          JG;
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                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotector; immunosuppressor; prédisposition; high blood pressure; cardiovasquiar disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                    (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                  30-DEC-1997;
                                                                                                                                                  30-DEC-1998;
                                                                                                                                                                              29-JUL-1999.
                                                                                                                                                                                                            W09937761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known polymorphism in the beta 2-adrenergic receptor gene as being linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta 2-adrenergic receptor DNA variant 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1523 CCCCGCCGTGGGTCCGCCCG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and individuals homozygous for Arg16 are more susceptible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
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                                                         Koepke K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                  97DE-1058401.
                                                                                                                                              98WO-DE03818
                                                                                                                                                                                                                                                             /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                replace(1666,c)
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(1633,a)
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                                                       Timmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB; 100.0%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                     nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
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                                                                                                                                                                                                                                                                                                                                          wild type amino acid sequence from an Gly residue to Arg residue" \,
                                                                                                                                                                                                                                      residue to Gln residue"
                                                                                                                                                                                                                                               wild type amino acid sequence from an
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Human beta2-adrenergic receptor gene variants, useful for

WPI; 1999-479048/40.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                            mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease;
                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metabolic illness; gene therapy; pharmaceutical intervention therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta 2-adrenergic receptor DNA variant 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for individuals is admirated for the property of the property of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA200779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ00779 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3451 BP; 789 A; 872 C; 897 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attention deficit disorder with hyperactivity, eating disorders, e.g. anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCGCCGTGGGTCCGCCCG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes novel variant human beta 2-adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
            /note=
                                      /*tag=
                                                                        replace(1666,c)
                                                                                                                                                                                                                                                                                    replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                                                                            replace(1568,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                           "This nucleotide differs from the wild type
"This nucleotide differs from the wild type
                                                                                                                           and results in a change in the corresponding wild type amino acid sequence from an Gly
                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                          nucleic acid sequence represented in AAZ00773"
                                                                                                     residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 2
Pred. No. 8.2;
                                                                                                  to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                        sequence represented in AAZ00773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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metabolic illness; gene

post-traumatic stress disorder; autonomous nervous system disease;

therapy; pharmaceutical intervention therapy

В

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RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bulimia; migraine; allergy; drug;
                                                           neuroprotector; immunosuppressor; predisposition; high blood pressure, cardiovascular disease; myocardial infarction; anxiety; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety attention deficit disorder with hyperactivity, eating disorders, e.g.
                                                                                                                                 Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                       Human beta 2-adrenergic receptor wild type DNA.
                                                                                                                                                                                                                                                                                07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                  AAZ00773;
                                                                                                                                                                                                                                                                                                                                                                                                              AAZ00773 standard; DNA; 3451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1523 CCCCGCCGTGGGTCCGCCCG 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3451 BP; 789 A; 873 C; 897 G; 892 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  individuals, including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AAZ00773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the autonomous nervous system, e.g. Bradbury-Eggleston, Sky-Drager
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-receptor agonists can be developed. Treatments can be optimized for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicting a change in weight, using body mass index, can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Riley-Day syndromes having selective noradrenergic-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anorexia nervosa and bulimia, or post-traumatic stress disorder. Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Fig 2a; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta2-adrenergic receptor gene variants, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoehe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09937761-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97DE-1058401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-DE03818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wild type amino acid sequence from an residue to Gln residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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AA200774" mutation
                                       AAZ00774" mutation
                                                                               mutation
                                                                                                                            AAZ00774" mutation
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                                                                                                                                                                                                                                                                                                                                                      mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                            /*tag=
                     /note=
                                                                  /*tag=
                                                                             replace(2110,a)
                                                                                                                                 /note= "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                         replace(1839,a)
/*tag= k
                                                                                                                                                                                                                                  replace(1666,g)
                                                          /note=
                                                                                                          /note=
                                                                                                                                                                                                                                                                                             replace(1633,g)
/*tag= i
                                                                                                                                                                                                                                                                    /note= "This mutation results in a change in the
corresponding wild type amino acid sequence
                                                                                                                                                                                                                                                                                                                                                   replace(1568,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This nucleotide differs from the wild type
                                                                                                                   /*tag=
                                                                                                                                                                                                             /note= "This mutation results in a change in the
                                                                                                                                                                                                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(159,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
         "This nucleotide differs from the wiid type
sequence in the sequence represented in
                                            "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                     "This mutation results in a change in the
                              Þ
                                                                                                                                                                                                                                                                                                                                                                                             "This mutation results in a change in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                              "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                          "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "This nucleotide differs from the wild type
                                                                                   corresponding wild type amino acid sequence from a Thr residue to Ile residue"
                                                                                                                                                                                                                                         from an Arg residue to Gly residue in the variant sequences represented in AAZ00774, AAZ00776, AAZ00777, AAZ00779 and AAZ00780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "This nucleotide differs from the wild type sequence in the sequence represented in
                                                                                                                                                                          variant sequences represented in AAZ00774 AAZ00776, AAZ00779"
                                                                                                                                                                                           corresponding wild type amino acid sequence from a Gln residue to Glu residue in the
                                                                                                                                                                                                                                                                                                                                                                   corresponding wild type amino acid sequence from an Arg residue to Cys residue in the variant sequences represented in AAZ00774,
                                                                                                                                                                                                                                                                                                            in the variant nucleotide sequences represented in AAZ00774 and AAZ00779" \,
                                                                                                                                                                                                                                                                                                                                                          AAZ00775, AAZ00777, AAZ00778 and AAZ00780"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence in the sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
  replace(2826,a)
                                      replace(2640,c)
                                                                                                                           replace(2078,t)
                                                                                                                                                                                                                                                                                                                                                                                                                     replace(1541,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replace(934,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(1221,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replace(1120,c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replace(245,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(565,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represented in
                                                                                                                                                                                                                                                          AAA38339
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                                                                                                                                                                                                 Qy
                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                               Best
                                                                                                              AAA38339;
                                                                                           21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoehe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998;
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Beta-adrenergic receptor-2 gene; regulatory region; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis; drug screening; treatment outcome; human; ds.

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CC pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are CC useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, the predistring the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-cc provides a basis for predicting the outcome of a treatment regimen. CC provides a basis for predicting the outcome of a treatment regimen. CC primers and probes for detecting a polymorphic site may be used as CC library arrays for high throughput screening. The genes, and the proteins CC drugs. Determination of an individual spolymorphic pattern reduces or calcium channel arror in selecting a treatment for a particular CC eliminates trial and error in selecting a treatment for a particular CC eliminates trial and error in selecting a treatment for a particular CC eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular CC identify polymorphic pattern so that the adverse results can be evaluated to correlated with a sub-nomination of that the adverse results can be
                                                                                                                 Matches
                                                                                                                                                                        Query Match
1523 CCCGCCGTGGGTCCGCCCG 1542
                                                                                                                                                                                                             Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                   correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. The present sequence represents the human beta-adrenergic receptor 2 gene regulatory region (GenBank M15169, J02728, M16106). The polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type I (ATI) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern -
                                                                                                                                                                                                                                                                                   .541C/T and 1568C/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 123-124; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norberg LT, Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EURO-) EURONA MEDICAL AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200022166-A2
                                                                                                                 Local Similarity es 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2000
                                                       1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                                                                                                                                                                                                                 identified are 934A/G, 987C/G, 1006A/G, 1120C/G,
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0104286
98US-0104302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-IB01678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            se, endothelin receptor type A and beta-adrenergic The method comprises determining the sequence at one
                                                                                                                                  100.0%;
                                                                                                                                                                  100.0%;
                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lindstrom PHR,
                                                                                                                                  Pred. No. 8.2;
                                                                                                                                                         Score 20;
                                                                                                           Mismatches
                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jonsson L;
                                                                                                           0;
                                                                                                                                                         Length 3451;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                 The polymorphic
/G, 1221C/T,
                                                                                                     0;
                                                                                                     Gaps
                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FT
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                                                                                                                                                25-0CT-2001.
                                                                                                                                                                                                        WO200179252-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarrhythmic; antiasthmatic; antidiabetic; tocolytic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference sequence for human beta2AR gene showing polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Polymorphic site 1 (PS1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace (565, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
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Stack CB,
Liggett SB;
                                     (GENA-) GENAISSANCE PHARM INC (UYCI-) UNIV CINCINNATI.
                                                                            13-APR-2000; 2000WO-US10125
                                                                                                     13-APR-2000; 2000WO-US10125
            Drysdale CM,
                                                                                                                                                                                              replace (2110, A)
/*tag= n
                                                                                                                                                                                                                                                                        /note= "Polymorphic site 10 (PS10)"
replace (1839, A)
/*tag= 1
                                                                                                                                                                                                                                               replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace (1541, T)
/*tag= g
                                                                                                                                                                                                                 /note= "Polymorphic site 12 (PS12)"
                                                                                                                                                                                                                                              /note= "Polymorphic site 11 (PSi1)" replace (2078, T)
                                                                                                                                                                                                                                                                                                                       /note= "Polymorphic site 9 (PS9)"
replace (1666, G)
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Polymorphic site 7 (PS7)" replace (1568, C)
                                                                                                                                                                                'note= "Polymorphic site 13 (PS13)"
                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                replace (1633, G)
                                                                                                                                                                                                                                                                                                                                                                              /product= "Beta2AR"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Polymorphic site 8 (PS8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Polymorphic site 6 (PS6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace (1221,
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Polymorphic site 2 (PS2)" replace (934, A)
                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                        1588..2829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Polymorphic site 5 (PS5)" replace (1221, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Polymorphic site 4 (PS4)" replace (1182, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace (879, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*taq=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Polymorphic site 3 (PS3)"
e (1120, C)
            Stephens JC,
          Nandabalan K,
          Judson
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RESULT 11 AAS18444

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AAA46128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic
                                                                                                                                                                                                                                                                                                                           allele-specific oligonucleotide primer; ss
                                                                                                                                                                                                                                                                                                                                                             obesity; diabetes; vascular disease; premature labour; migraine;
                                                                                                                                                                                                                                                                                                                                                                              Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR; chromosome 5q31(12); disease predisposition; asthma; hypertensi congestive heart failure; ischemic heart disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta2 adrenergic receptor beta2AR T allele-specific primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to polymorphisms and haplotypes of the human beta2-adrenergic receptor (beta2-AR) gene located on chromosome 5931-32, and methods for haplotyping and/or genotyping the beta2AR gene in an individual. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers for detecting the beta2AR gene polymorphisms. The beta2AR gene polymorphisms are useful in studying the expression and biological function of beta2AR, and for develoning driver transition of beta2AR, send for develoning driver transition of beta2AR.
                                           WPI; 2000-400107/34.
                                                                                                               (UYCI-) UNIV CINCINNATI
                                                                                                                                                   25-NOV-1998;
                                                                                                                                                                                       24-NOV-1999;
                                                                                                                                                                                                                         02-JUN-2000
                                                                                                                                                                                                                                                             W0200031307-A1
                                                                                                                                                                                                                                                                                                                                                      anaphylaxis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for therapeutic purposes such as treating disorders affected by expression or function of beta2AR such as congestive heart failure, arrhythmia, ischaemic heart disease, hypertension, migraine, asthma, chronic obstructive pulmonary disease (COPD), obesity, diabetes and premature labour. The method is useful for determining the frequency of a beta2AR genotype or haplotype in a population. The present sequence represents a reference sequence for the human beta2AR gene which shows
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA46128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA46128 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated beta 2-adrenergic receptor polynucleotide, useful for studying expression and biological function of receptor and for developing drugs targeting receptor, comprises polymorphism of adenosine at PS2 and thymine at PS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAU10763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-061968/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for developing drugs targeting this receptor. They are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                              chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                 98US-0109886
                                                                                                                                                                                     99WO-US27963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB:
Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                   asthma; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
              Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure.
                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 5q31(12); disease predisposition; asthma; hypertension; congestive heart failure; ischemic heart disease; arrhythmia; obesity; diabetes; vascular disease; premature labour; migraine; anaphylaxis; chronic obstructive pulmonary disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphism is found in the 5' leader sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-angonists and beta-antagonists, and is likely to influence their predisposition to astima, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and determine the best treatment.
                                                                                                                                                                                                                                                                                                                                       (UYCI-) UNIV CINCINNATI
                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200031307-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human beta2 adrenergic receptor beta2AR gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA38785 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which is located on chromosome 5q31 (12). The gene has two different alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader sequence, which encodes a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 0 A; 10 C; 7 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is an allele-specific oligonucleotide primer for the T allele of the human beta2 adrenergic receptor (beta2AR) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 11; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCCGCCGTGGGTCCGCCTG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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             This sequence represents the human beta2-adrenergic receptor gene, and is amplified by the primers of the invention. The primers are non-self hybridising; contain at least 15 nucleotides (nt) and has a melting temperature 50-85 deg. C. Each pair of primers is: non-cross-hybridising; anneals to two distinct segments (separated by at least 400 nt); and generates a homogeneous population of gene segments in a polymerase chain reaction (PCR). At least one primer in the pair can extend a 3'-end
                                                                                                                                                                     Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                     WPI; 1999-327357/27.
                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                10-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09924454-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta2 adrenergic receptor; genetic variation identification; hypertrophy; disease diagnosis; hypertension; prostatic disease; pulmonary disorder; asthma; peripheral vascular disorder; neuropsychic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence, which encodes a peptide which regulates expression of the beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, isohemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlphalB-adrenergic receptor; human; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endocrine-metabolic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human beta2-adrenergic receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX61116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60 BP; 6 A; 24 C; 21 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a fragment of the T allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome 5931 (12). The gene has two different allele, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determine the best treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Figure 2; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                    oligonucleotides for amplifying adrenergic receptor genes
complementary to a template sequence in a DNA polymerase
                                                                                                                                                                                                                                                                                      Herrmann V, Insel PA;
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95.0%;
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Pred. No. 5
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Best Local :
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                                                                                                                                                                                                             polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern
                                                                                                                                                                                                                                            Assessing cardiovascular status in humans involves comparing test
                                                                                                                                                                                                                                                                                                             Norberg LT,
                                                                                                                                                                                                                                                                                                                                                                          14-OCT-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-adrenergic receptor-2 gene; coding region; polymorphism; polymorphic marker; cardiovascular disease; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atheroscle stroke; prognosis; drug screening; treatment outcome; human; ds.
                                                                                                                                                                                                                                                                                                                                          (EURO-) EURONA MEDICAL AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA38340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human beta-adrenergic receptor-2 coding region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of genetic alterations not previously amenable to routine, automated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reaction. The primers are used to amplify segments of the alphaib and beta2 adrenergic receptor genes, particularly to identify genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 large-scale sequencing analysis.
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                                                                                                                                                                                                                                                                                                           Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB01678
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95.0%;
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                        Jonsson L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atherosclerosis;
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or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to

receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one

genes encoding angiotensin-converting enzyme (ACE), angiotensin II status in an individual and to newly identified polymorphisms in the The invention relates to a novel method of assessing the cardiovascular Disclosure; Page 124-125; 126pp; English.

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                                                                                                                                                                                                                                              CC primers and probes for detecting genetic polymorphisms or in molecular CC library arrays for high throughput screening. The genes, and the proteins CC they encode are useful in the screening of potential cardiovascular CC drugs. Determination of an individual's polymorphic pattern reduces or CC eliminates trial and error in selecting a treatment for a particular CC individual cardiovascular patient. It also provides the ability to CC eliminate patients from clinical trials who are predicted to be CC conformed to the conformation of the treatment regimen. Adverse results in an early trial can be evaluated to CC identify polymorphic patterns so that the adverse results can be CC correlated with a sub-population of the test population, permitting CC exclusion of such sub-populations from the treatment group. Beneficial CC drugs can be approved for use in the appropriate population, thereby CC decreasing the number of patterns required for a clinical trial, which in CC sequence represents the human beta -adrenceryic receptor 2 gene CC coding region (GenBank Y00106,9293708). The polymorphic sites identified CC are 839A/G, 878C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G, 2032A/G,
                                                                                                              Matches
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                                                                                                                                                                                                    Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;
729 CCCCGCCGTGGGTCCGCCTG 748
                                                 1 CCCCGCCGTGGGTCCGCCCG 20
                                                                                                         19; Conservative
                                                                                                                            92.0%;
95.0%;
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                                                                                                                         Score 18.4; DB 21; Length 2305; pred. No. 40;
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## ALIGNMENTS

CUSSION Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds.

CCESSION BC012481.1 GI:15214693
WMCDLS
WMCDLS
WMCDLS
BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
AUTHORS
Strausberg, R.
Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (WCC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
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Contact: MGC help desk
Email: cgapbs-remail.nlh.gov
Tissue Procurement: DCTD/DTP

FEATURES

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Query Match
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                                                                                                                                                                              Schofield,P.R., Rhoe,L.M. and Peralta,E.G. Primary structure of the human beta-adrenergic receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                   Human gene for beta-adrenergic receptor (beta-2 subtype).
                                                         Submitted (20-OCT-1987
                                                                             Direct Submission
                                                                                                    Schofield, P.R.
                                                                                                                                                                Nucleic Acids Res. 15 (8),
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK plate: 28 Row: k Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gl: 178203.
                                                                                                                                                                                                                                                                                                                                          beta-adrenergic receptor.
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villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garci
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/db_xref="g1:15214694"
/translation="MgQPGNGSAFLLAENGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
/translation="MgQPGNGSAFLLAENGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
LAIVFGNVLVITAIAKEEKLQTVTNYFITSLACADLVMGLAVVEFGAAHILMKWNTFG
RWCEEWTSIDVLCYTASIETLCVIAVDRYFAITSPERVQSLLTKNKARVIILMVHV
SGLTSBLPLQMHWYRATHQEAINCYANDTCOEDFTYNQAYAJASSTYLKFUKYFV
YSRVFQEAKRQLQKIDKSEGRHYQNLSQVEGDGRTGHGLARSSKFCLKEHKALKTLG
ILMGTFTLCWLPEFIVNIYHVIQDNLLEKEVILLMWIGYVNSGENPLIYCRSPDERI
                             Location/Qualifiers
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222. .1463
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/db_xref="taxon:9606"
/clone="MGC:21367 IMAGE:4538187"
/tion:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Prostate, adenocarcinoma."
/clone_lib="NIH_MGC_91"
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Sequence 1 from Patent W09937761.
AX022517
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                                                                                                                                                                                                                                                                                                                                 unidentified
unclassified.
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                                                                                                                                                                       MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                                              HOEHE MARGRET (DE); KOEPKE KARLA
                                                                                                                                                                                                                                                       Novel sequence variants of the human beta2-adrenergic receptor gene
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                                                                /organism="unidentified"
/db_xref="taxon:32644"
871 c 892 g 89
                                                                                                                                1. .3451
                                                                                                                                                     Location/Qualifiers
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1712. 1774
/note="membrane spanning domain VII"
616 c 649 g 545 t
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IIMGTFTLCWLPFFIVNIYHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGBQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
SGLTSFLPIQMHWYRATHOEAINCYANETCCDPFTNQAYALASSIVSFYVPLVIMVFV
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1247. .1315
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/db_xref="GI:29371"
/db_xref="SWISS-PROT:P07550"
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/db_xref="taxon:9606"
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Hoehe, M., Koepke, K. and Timmermann, B.
Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                           HOBHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT EUER MOLEKULA (DE); TIMMERMANN BERND (DE)
                                                                                                                                                                                                                                          Patent: WO 9937761-A 4 29-JUL-1999;
                                                                                                                                                                                                                                                            and use
                                                                                                                                                                                                                                                                                                                               unidentified
                                                                                                                                                                                                                                                                                                                                             unidentified
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                                                                                                                                                                                                                                                                                                                 unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 9937761-A 2 29-JUL-1999;
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Hoehe, M., Koepke, K. and Timmermann, B.
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                                                                                                                                                          /organism="unidentified"
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AX022523
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              ACCESSION
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                       Human beta-2-adrenergic receptor gene, complete cds
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              J02960
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HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERMANN BERND (DE)
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J02960.1 GI:178203
                                          HUMADRBRA
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Sequence 7 from Patent W09937761
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                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
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HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERMANN BERND (DE)
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Sequence 5 from Patent WO9937761.
AX022521
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Hoehe, M., Koepke, K. and Timmermann, B.
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PAT 07-SEP-2000

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DEFINITION ACCESSION
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Sequence 354 from Patent WO0148245. AX204248
                                                                                                                                                                                                                                                                            1 bp upstream of EcoRI site; chromosome 5q31-q32
                                     AX204248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                           Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3458)
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                                                                                                                                                                                                                                                                                                      777 a
                                                                                                                                                                                                            Conservative
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led by L.J.Emorine, 25-AUG-1987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="beta-2 adrenergic receptor"
/protein_id="AAA88017.1"
/db_xref="GI:178204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ADRB2"
1264. .2505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="beta-2-adrenergic receptor mRNA (alt.)" 1264...2505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1064.
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GEECLAPSRLPACHWPKVPVRHGEGSSPKVLCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="unknown protein"
/protein_id="AAA88016.1"
/protein_id="AAA88016.1"
/db_xref="G1:560762"
/translation="MFEREYTGLPGVCWEGSIISARVRQVRSTQMETSVSVSLWMPPS
                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
LAIVFGNVLVITAIAKFERLQTVTNYEITSLACADLVMGLAVVPFGAAHILMKMWTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="beta-2-adrenergic receptor mRNA (alt.)"
1055. .3057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRVETFCVCHHVFVLLGASVFVSGRVSVLDRGDFVPDGFCVRARASVHVGELGGCVSV
SMAVVRYKSEHVCQGVFVPVCACLGGHSRFLPNVGQCRCAALCLETSSRAGAQGRQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="epidermis"
277. .1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="beta-2-adrenergic receptor mRNA (alt.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GDB:G00-120-541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ADRB2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="H-beta-R-[9,10,11]."
/cell_line="A431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="5q31-q32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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155 CCCGCCGTGGGTCCGCCG 174
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                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[bases 1 to 1970]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 bp
Sequence 8 from patent US 6273893
ARI64456
Chung, F.Z., Lentes, K.U., Gocayne, J., Fitzgerald, M., Robinson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Absorbable rivet/pin applier for use in surgical procedures Patent: US 6273893-A 8 14-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 230) McAllen, J. III, Overaker, D.W. and Cooper, K.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methods of use thereof
Patent: WO 0148245-A 354 05-JUL-2001;
                                                                                                                          beta-adrenergic receptor.
                                                                                                                                                    X04827.1 GI:29372
                                                                                                                                                                                           Human mRNA for brain beta-adrenergic
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1 (bases 1 to 51)
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Accession number cg43040273"
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91 c 70 g
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                                                                                                                                                                                                                                                                                                                                                                                                                      92.0%; Score 18.4; DB 6; 95.0%; Pred. No. 5.6e+02;
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95.0%;
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Pred. No. 7.8e+02;
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RESULT 12
AX022519
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                                 and use thereof
Patent: WO 9937761-A 3 29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                              3451 bp
Sequence 3 from Patent WO9937761
AX022519
HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT FUER
                                                                                           Novel sequence variants of the human beta2-adrenergic receptor
                                                                                                                                    Hoehe, M., Koepke, K. and Timmermann, B.
                                                                                                                                                                                                                                          unidentified
                                                                                                                                                                                                                                                                            unidentified
                                                                                                                                                                                                           unclassified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substantial corrections are reported in [2]
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                                                                                                                                                                      (bases 1 to 3451)
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965..9
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508 c 482 g
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1970
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1491. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="pot.
1952. .1957
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IMGTFTLCWLFFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="pot. glucocorticoid-responsive element"
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95.0%;
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Pred. No. 3.
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RESULT 14
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AUTHORS
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AX022522
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                                                                            Avalon Pharmaceuticals (US)
                                                                                                          gene sets
                                                                                                                    Cancer gene determination and therapeutic screening using signature
                                                                                                                                   Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
                                                                                                                                                                                                                 Homo sapiens
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HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERWANN BERND (DE)
                                                                                             Patent:
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                              AX332732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and use thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel sequence variants of the human beta2-adrenergic receptor gene
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Hoehe, M., Koepke, K. and Timmermann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
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Location/Qualifiers
                                                                                                                                                                                Mammalia; Eutheria; Primates; Catarrhini;
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   Ω
                                                                                         WO 0194629-A 3241 13-DEC-2001;
                                                         Location/Qualifiers
 /db_xref="taxon:9606"
873 c 895 g
                               /organism⇔"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:32644"
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872 c 897 g
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DEFINITION
ACCESSION
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AX334116
Search completed: November 2, 2002, 16:50:27 Job time: 390.636 secs
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                                                                                                                                                          Query Match 92.0%; Score 18.4; DB 6; Length 3451; Best Local Similarity 95.0%; Pred. No. 3.1e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps
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Patent: WO 0194629-A 4625 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
790 a 873 c 895 g 89
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Y00106 Human gene AX022517 Sequence AX022518 Sequence

BC012481 Homo sap

AX022520 Sequence AX022521 Sequence

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                      Result
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                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                      and is derived by analysis of the total score distribution.
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Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Submitted (15-AUG-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2063)
                                                                                                                                                    Homo sapiens, Similar to adrenergic, beta-2-, receptor, surface, clone MGC:21367 IMAGE:4538187, mRNA, complete cds. BC012481
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Ti: ue Procurement: DCTD/DTP
                                                                                                                                    MGC
                          NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                Strausberg, R.
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AR105183 Sequence AX333697 Sequence M94172 Human N-typ I13706 Sequence 12 K02212 Human alpha AC017698 Drosophil

AC019671 Drosophil AC095779 Rattus no Continuation (2 of

AC013655 Homo sapi 249154 Human DNA

AP001900 Homo sapi AL132708 Human chr

AR118079 Sequence AR022379 Sequence AR063882 Sequence AR067882 Sequence

M94173 Human N-typ M22618 Serratia ma

AR105184 Sequence AR067883 Sequence

AR022380 Sequence AR063883 Sequence A22938 H.sapiens m AR150755 Sequence AB020986 Canis fam E59801 Canine obsi

I12881 Sequence 14 AK055768 Homo sapi

U10900 Rattus norv I12880 Sequence 12

A22950 H.sapiens m AR150761 Sequence

AB025351 Rana cate

AC095307

Rattus no

AC025128 Homo sapi AC091404 Sus scrof

J02960 Human beta-AX022523 Sequence

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PRI 20-AUG-2001

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 178203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garc
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muzny,D.M., Gibbs,R.A.
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                                          Direct Submission
Submitted (20-OCT-1987)
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                                                                                                                                                        1 (bases 1 to 2305)
Schoffield,P.R., Rhee,L.M. and Peralta,E.G.
Primary structure of the human beta-adrenergic receptor gene
Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                                                                                                                                                                                                                                                                                      beta-adrenergic receptor.
                                                                                                                                                                                                                                                                                                                                                                             Y00106.1 GI:29370
                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene for beta-adrenergic receptor (beta-2 subtype).
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                                                                                          Schofield, P.R.
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TVPSDNIDSPGRNCSTNDSLL"
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NEWCEEWTSIDVLCVTASIETLCVIAVDRYEAITSPEKYQSLLTKNKARVIILMVWIV
SGLTSELPIQMHWYRATHQEAINCYANETCCDEFTNQAYAIASSIVSEYVPLVIMVEV
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surface"
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/tissue_type="Prostate, adenocarcinoma."
/clone_lib="NHH_MGC_91"
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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/db_xref="GI:15214694"
/translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGTVMSLTV
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HOEHE MARGRET (DE); KOEPKE KARLA (DE);
MOLEKULA (DE); TIMMERNANN BERND (DE)
                                                                                                                                                                                                 and use
                                                                                                                                                                                                                  Hoehe,M., Koepke,K. and Timmermann,B. Novel sequence variants of the human beta2-adrenergic receptor gene
                                                                                                                                                                                                                                                                                           unidentified
                                                                                                                                                                                                                                                                                                                                                 AX022517.1 GI:10046115
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 from Patent W09937761. AX022517
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17.2..1774
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1007. .1078
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                                                                      /db_xref="taxon:32644"
                                                                                        /organism="unidentified"
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HOEHE MARGRET (DE); KOEPKE KARLA (DE); MAX DELBRUECK CT
MOLEKULA (DE); TIMMERMANN BERND (DE)
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Sequence 4 from Patent W09937761.
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Sequence 7 from Patent WO9937761.
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J02960
J02960.1 GI:178203
                             Human beta-2-adrenergic receptor gene, complete cds
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Hoehe, M., Koepke, K. and Timmermann, B.
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                                                                                                                                                                                                                                                                                 Local
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Homo sapiens clone RP11-307E16, LOW-PASS SEQUENCE SAMPLING AC025128
                                                                                                                                                                                                                                                           l Similarity 100.0%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                               1 bp upstream of EcoRI site; chromosome 5q31-q32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and computer-readable copy of sequence [1] kindly provided by L.J.Emorine, 25-AUG-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88041037
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                                              AC025128
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                                                                                                                                                                                                                                                                                                                                                                                                                     AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                              TIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GDB:G00-120-541"
/translation="MGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
LAIVEGNVLVITALAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-2 adrenergic receptor"
/protein_id="AAA88017.1"
/db_xref="GI:178204"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="beta-2-adrenergic receptor mRNA (alt.)"
1264. .2505
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QRVFTFCVCHHVFVLLGASVFVSGRVSVLDRGDFVPDGFCVRARASVHVGELGGCVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAA88016.1"
/db_xref="GI:560762"
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/cell_line="A431"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ADRB2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This record contains 36 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Low-pass sequence sampling is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 31740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 31740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: L7794
Center clone name: 307_E_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead
                                                                 4.395 5145: contig of 751 bp in length 5146 5245: gap of 100 bp 5246 6045; contig of 751 bp in length 6046 6146
                                                                                                                                                                           4294: contig of 758 bp in length 4295 4394: gap of 100 bp 5145: contin of 758 5146 sour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      800 899: gap of 100 bp
900 1693: contig of 794 bp in length
1694 1793: gap of 100 bp
1794 2579: contig of 786 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2580 2679:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- Genome Center
100 bp in length 6045: contig of 800 bp in length 100 bp contin of 5: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                          25/9: contig of 786 bp in length
79: gap of 100 bp
3436: contin of -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is updated,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         799:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 799 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choepel, Y., Colangelo, M., Collins, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , FitzHugh,W., Gage,D.
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linear

HTG 19-APR-2001

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FEATURES
                                                                                                                                                                                                 BASE COUNT
                                                                                                  Matches
                                                                                                                  Query Match
Best Local
                        8257 GTCCGCCTGCTGAGG 8243
                                                                                                                                                                                                                                                                                              source
                                                          1 GTCCGCCTGCTGAGG 15
                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            29996 30095:
                                                                                                                                                                                                                                                                                                                                                                                                                            29106 29205: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20238 20337: gap of 100 bp
20338 21119: contig of 782 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16702 16801:
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15895 16701: con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17588 17687: gap of 100 b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19355 19454:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7844 7943:
                                                                                                                                                                                           /clone="RP11-307E16"
/clone_lib="RPCI-11 Human Male BAC"
/154 c 6162 g 7609 t 3664 c
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14128: gap of 772 bp in length 1500: contig of 772 bp in length 1500: gap of 100 bp 15794: contig of 794 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11453: gap of 100 b
12246: contig of 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12346:
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27317: contig of 793 bp
27417: gap of 100 bp
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23749: contig of 777 bp
3849: gap of 100 bp
24643: contig of 794 bp
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....: gap of
20237: ~
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10452: cont
                                                                                                                    100.0%;
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13148: contig of 802 bp
                                                                                                                                                                                                                                                                                                                                                                  29995: contig of 790 bp
100 bp
30893: contig of 798 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                             28208: contig of 791 bp in length
100 bp
29105: contig of 797 bp in length
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21995: contig of 776 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73: gap of 100 bp
19354: contig of 781 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25561
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22872: contig of 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14028: contig of 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7843:
                                                                                                                                        100.0%;
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17587: contig of 786 bp in length
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gap of 100 b
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contig of 783 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 100 bp
contig of 770 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p of 100 bp contig of 818 bp
                                                                                                                                                                                                                                                                                                                                p of 100 bp
contig of 747 bp
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                                                                                                  0;
                                                                                                                  Score 15; DB 2;
Pred. No. 5.9e+02;
                                                                                                  Mismatches
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                                                                                                                                                                                               3664 others
                                                                                                                                    Length 31740;
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                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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JOURNAL
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                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-APR-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maštrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantripop,S., Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Ho,S.-L., Idol,J.R., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B., Masiello,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa clone RP44-74011, WORKING DRAFT SEQUENCE, 6 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC091404.1 GI:13677075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 158755)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrota
                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 158755)
                                                                                              3650
3750
13663
13763
13763
32624
32724
55172
55272
                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 10.68x in Q20 bases; agarose-fp Quality coverage: 8.70x in Q20 bases; pulse-field-gel Quality coverage: 10.39x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 155345 bases at least Q40 Consensus quality: 156172 bases at least Q30 Consensus quality: 156597 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 154000; agarose-fp
Insert size: 189000; pulse-field-gel
Insert size: 158255; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: akp
Center clone name: 074011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov
/organism="Sus scrofa"
                                    Location/Qualifiers
                                                                                                            3649: contig of 3649 bp in length
3749: gap of unknown length
13662: contig of 9913 bp in length
13762: gap of unknown length
32623: contig of 18861 bp in length
32723: gap of unknown length
55171: contig of 22448 bp in length
55271: gap of unknown length
                        .15875
                                                        86367: contig of 31096 bp in 86467: gap of unknown length 158755: contig of 72288 bp in

    Summary Statistics

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158755 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC095307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
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15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carte, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, C., Chard, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Davis, C., Chare, C
                                                                                                                                                                                   Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gablsi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunarathe,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-23A17, *** SEQUENCING IN PROGRESS ***, 60 unordered pieces.
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.
                                                              Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Nohabba
Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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86468. .158755
/note="assembly_fragment"
, 38951 c 37930 g 39519
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13763. .32623
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Pred. No. 5.3e+02;
); Mismatches 0; Indels 0;
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                                                                               Newtson, N.,
                                                                                                                Mohabbat, K.,
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pul.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Telfrod, B., Thomas, N., Tangly, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R. Wall,R., Wany,S., Ward-Moore,S., Warren,R., Washington,C., Wathington,S., Williams,G., Williamson,A., Weczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D. Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15625861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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* is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-MAR-1999) Kenkichi Sugimoto, Niigata University, Faculty of Graduated School of Science and Technology; Igarashi Nino-cho 8050, Niigata, Niigata 950-2181, Japan (E-mail:sugimoto@sc.niigata-u.ac.jp, Tel:81-25-262-6151,
Similarity 100 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 706)
Sugimoto, K. and Saito, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax:81-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning and characterization of amphibian cold inducible
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                                                                                                                                                                                GFFRGGRGRGGGGYGGSSRFDNRSGGGYGGWIPDYYSSGRESSYGDRSAGGRSYRDSY
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                                                                                                                                                                                                                                                          /protein_id="BAA88978.1"
/db_xref="GI:6682989"
                                                                                                                                                                                                                                                                                                             /product="BFCIRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rana catesbeiana"
/db_xref="taxon:8400"
                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
                                                                                                                                                                                                                               translation="MSCDEGKLFVGGLSFDTDEQCLETVFSKYGQIQEVVVVKDRETK"
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93.3%; Score 14; DB 5; I
100.0%; Pred. No. 2.9e+03;
tive 0; Mismatches 0;
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Pred. No. 5.3e+02;
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                                                                                                                                                                      14; Conservative
I12881 2470 bp
Sequence 14 from patent US 5429921.
I12881 GI:910858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
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Franz,J., Weingartner,B., Unterbeck,A. and Rae,P.
Tissue-specific human neuronal calcium channel subtypes and their
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Sequence 17 from patent US 6229000
AR150761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Franz,J., Weingaerther,B., Unterbeck,A. and Rae,P. Calcium channel subtype specific of human neuronal tissue and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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A22950.1 GI:1247418
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                                                                                                                                                                                                                                                                                                   Patent: US 6229000-A 17 08-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                       Unknown
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/db_xref="taxon:9606"
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100.0%; Pred. No. 2.8e+03;
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                                              1739 TCCGCCTGCTGAGG 1752
                                                                            2 TCCGCCTGCTGAGG 15
                                                                                                                                                                                                                                                                                                           l (bases 1 to 2470)
Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F. and Brenner,R.
                                                                                                                                                                                                                                                               Patent: US 5429921-A 14 04-JUL-1995;
                                                                                                                                                                                                                                                                                               Assays for agonists and antagonists of recombinant human calcium
                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
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